

GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: April 11, 2006, 02:03:38 ; Search time 112.845 Seconds
(without alignments)
1608.075 Million cell updates/sec
Title: US-09-037-657-13
Perfect score: 2251
Sequence: 1 MPAGRPGVQAQRRPRRL.....WRAMQKSHKTRNQVLPAKL 413
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2251	100.0	413	2 AAW55011	Novel hae
2	2251	100.0	413	3 AAY93658	Aay93658 A murine
3	2251	100.0	413	4 AAS00820	Aae00820 Murine ha
4	2226.5	98.9	425	2 AAW55012	Novel hae
5	2226.5	98.9	425	3 AAY93659	Aay93659 A murine
6	2226.5	98.9	425	4 AAS00821	Aae00821 Murine ha
7	2222.5	98.7	425	2 AAW59804	Aay59804 Nucleotid
8	2222.5	98.7	425	2 AAY26337	Murine U4
9	2197.5	97.6	425	2 AAW70862	Rat Zcyto
10	2134.5	94.8	416	2 AAY29780	Mouse DNA
11	2119	94.1	407	3 AAB19589	Aab19589 Mouse cyt
12	2119	94.1	407	4 AAB36648	Mouse cyt
13	2119	94.1	407	7 ADC07180	Mouse cyt
14	2119	94.1	407	8 ADT90845	Mouse cyt
15	2119	94.1	407	8 ADT61033	Mouse cyt
16	2119	94.1	407	9 ADT57158	Mouse cyt
17	2119	94.1	407	9 ADZ65015	Mouse NR6
18	2118.5	94.1	405	2 AAY15214	Aay15214 Amino aci
19	2118.5	94.1	405	3 AAY44839	Mouse orp
20	2114.5	93.9	410	2 AAY29779	Human DNA
21	2114.5	93.9	410	3 AAB19588	Human cyt
22	2114.5	93.9	410	4 AAB36647	Human cyt
23	2114.5	93.9	410	7 ADC07179	Human cyt
24	2114.5	93.9	410	8 ADT90844	Human cyt

ALIGNMENTS

RESULT 1					
AAW55011					
ID	AAW55011	standard; protein; 413 AA.	410	8	ADT61032 Human cyt
XX			410	9	ADY57157 Human cyt
AC	AAW55011;		410	9	ADZ65014 Human NR6
DT	29-SEP-1998	(first entry)	425	2	AAW70861 Allelic v
XX			425	2	AAE00826 Murine ha
DE	Novel haemopoietin receptor NR6.1 protein.		426	4	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
KW	Haemopoietin receptor; cell proliferation; cell differentiation; cancer;		422	2	AAE00826 Murine ha
KW	cell survival; therapeutic; neuronal proliferation; drug screening;		422	2	AAE00826 Murine ha
KW	Mouse.		422	2	AAE00826 Murine ha
OS	Mus sp.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
PN	WO9811225-A2.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
PD	19-MAR-1998.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
PF	11-SEP-1997; 97WO-GB002479.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
PR	11-SEP-1996; 96AU-00002246.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
XX	(AMRA-) AMRAD OPERATIONS PTY LTD.		422	2	AAE00826 Murine ha
XX	(DZIE/) DZIEGLEWSKA H E.		422	2	AAE00826 Murine ha
PI	Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;		422	2	AAE00826 Murine ha
PI	Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;		422	2	AAE00826 Murine ha
DR	WPI: 1998-260970/23.		422	2	AAE00826 Murine ha
XX	N-PSDB; AAV27140.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
PT	New isolated haemopoietin receptor - used for developing products for		422	2	AAE00826 Murine ha
PT	modulating proliferation, differentiation and survival of cells, e.g.		422	2	AAE00826 Murine ha
XX	neural cells.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
PS	Claim 14; Page 77-81; 182pp; English.		422	2	AAE00826 Murine ha
XX			422	2	AAE00826 Murine ha
CC	The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.		422	2	AAE00826 Murine ha
CC	Interaction between the novel HR and a ligand facilitates proliferation,		422	2	AAE00826 Murine ha
CC	differentiation and survival of a wide variety of cells. The HR and it's		422	2	AAE00826 Murine ha
CC	derivatives can be used for modulating the activity of the receptors e.g.		422	2	AAE00826 Murine ha
CC	to regulate development, maintenance or regeneration in an array of		422	2	AAE00826 Murine ha
CC	different cells and tissues in vitro and in vivo. They can be present in		422	2	AAE00826 Murine ha
CC	therapeutics used for modulating neuronal proliferation, differentiation		422	2	AAE00826 Murine ha
CC	and survival. The products can also be used for detection and diagnosis,		422	2	AAE00826 Murine ha

PD 19-APR-2001.
 XX 06-OCT-2000; 2000WO-AU001216.
 XX 08-OCT-1999; 99AU-00003327.
 PR 12-MAY-2000; 2000AU-00007489.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
 PI Nakata Y, Hasegawa M;
 PI WPI; 2001-281978/29.
 DR N-PSDB; AAD04192.
 XX New biologically active complex comprising NR6 and cardiotrophin-like-
 PT cytokine, for facilitating proliferation, differentiation and/or survival
 PT of a cell.
 XX Claim 25; Page 76-77; 123pp; English.
 XX The present invention relates to a biologically active complex comprising
 CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The
 CC complex is useful in the manufacture of a medicament for the treatment
 CC and/or prophylaxis of a subject, as it is involved in facilitating
 CC proliferation, differentiation and/or survival of a cell. The complex or
 CC its components have neurotrophic activity. The present sequence is murine
 CC haemopoietin receptor, NR6.1 isoform. The NR6.1 represents the NR6 splice
 CC variant obtained due to alternative mRNA splicing
 CC
 CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
 XX Sequence 413 AA;
 SQ
 Query Match 100.0%; Score 2251; DB 4; Length 413;
 Best Local Similarity 100.0%; Pred. No. 2.5e-186; Mismatches 0; Indels 0; Gaps 0;
 Matches 413; Conservative 0;
 QY 1 MPAGRPGVQAQARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60
 Db 1 MPAGRPGVQAQARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60
 QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 Db 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 Db 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240
 Db 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240
 QY 241 PPDVHVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYVEDSVDMKVDDVSNQTSR 300
 Db 241 PPDVHVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYVEDSVDMKVDDVSNQTSR 300
 QY 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGVCBPRGGE 360
 Db 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGVCBPRGGE 360
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLVDQWRAWMQKSHKTRNOVLPAKL 413
 Db 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLVDQWRAWMQKSHKTRNOVLPAKL 413
 RESULT 4
 ID AAW55012
 XX AAW55012 standard; protein; 425 AA.
 AC AAW55012;
 XX

DT 29-SEP-1998 (first entry)
 XX Novel haemopoietin receptor NR6.2 protein.
 XX Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening;
 KW Mouse.
 XX Mus sp.
 XX WO9811225-A2.
 XX 19-MAR-1998.
 XX 11-SEP-1997; 97WO-GB002479.
 XX 11-SEP-1996; 96AU-00002246.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA (DZIE/) DZIEGLEWSKA H E.
 XX Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;
 PI Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;
 XX WPI; 1998-260970/23.
 DR N-PSDB; AAV27141.
 XX New isolated haemopoietin receptor - used for developing products for
 PT modulating proliferation, differentiation and survival of cells, e.g.
 PT neuronal cells.
 XX Claim 15; Page 84-87; 182pp; English.
 XX The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and its
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening
 XX
 SQ Sequence 425 AA;
 Query Match 98.9%; Score 2226.5; DB 2; Length 425;
 Best Local Similarity 98.8%; Pred. No. 3.5e-184; Mismatches 2; Indels 3; Gaps 1;
 Matches 409; Conservative 2;
 QY 1 MPAGRPGVQAQARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60
 Db 1 MPAGRPGVQAQARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSILQ 60
 QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 Db 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 Db 121 ARDGSILAGSCLYVGLPPEKPNISCSRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240
 Db 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLVDLVVTTDP 240
 QY 241 PPDVHVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYVEDSVDMKVDDVSNQTSR 300
 Db 241 PPDVHVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYVEDSVDMKVDDVSNQTSR 300
 QY 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGVCBPRGGE 360
 Db 301 LAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGVCBPRGGE 360

QY 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
 DB 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 414

RESULT 5
 ID AAY93659 standard; protein; 425 AA.
 AC AAY93659;
 DT 25-SEP-2000 (first entry)
 DE A murine hemopoietin receptor NR6.2 polypeptide.
 KW Hemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation;
 KW hemopoietic progenitor cell; cancer; apoptosis; postnatal survival;
 KW suckling; postnatal baby; foetal testing.
 OS Mus musculus.
 PN WO200035471-A1.
 PD 22-JUN-2000.
 PF 17-DEC-1999; 99WO-AU001119.
 PR 17-DEC-1998; 98AU-00007762.
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PI Alexander WS, Metcalf D;
 DR WPI: 2000-442273/38.
 DR N-PSDB; AAR46792.
 XX Administering the hemopoietin receptor NR6 is used to modulate production
 of hemopoietic progenitor cells and facilitate postnatal survival of
 mammals by inducing or promoting suckling.
 PS Claim 5; Page 73-74; 77pp; English.
 XX The present sequence represents a murine haemopoietin receptor NR6 (CLF-
 1) polypeptide. The specification describes a method for the treatment or
 prophylaxis of disease conditions associated with dysfunctional
 haemopoietic regulation. The method comprises modulating the production
 of hemopoietic progenitor cells in a mammal by administration of NR6.
 CC Decreasing production of progenitor cells may be used in the treatment of
 cancer or to induce apoptosis of particular cell types. Increasing
 production of progenitor cells is used to facilitate postnatal survival
 in mammals by inducing or promoting suckling. Potential disease
 conditions may be identified by monitoring NR6 production in postnatal
 babies or allowing expectant mothers to undergo foetal testing. Low NR6
 levels can then be treated immediately

Query Match 98.9%; Score 2226.5; DB 3; Length 425;
 Best Local Similarity 98.8%; Pred. No. 3.5e-184;
 Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRGQVQAASARRPRPLSSLLWSPLLCLVGVPRGGGAHTAVISPODPTLLIGSSLQ 60
 DB 1 MPAGRGQVQAASARRPRPLSSLLWSPLLCLVGVPRGGGAHTAVISPODPTLLIGSSLQ 60
 QY 61 ATCSIHGDTGTAEGLYWTLNGRPLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTGTAEGLYWTLNGRPLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSLVGLVPPKPFNISCWSRNKDLTCRWTPGAGETFLHTNYSILKYLWR 180
 DB 121 ARDGSILAGSLVGLVPPKPFNISCWSRNKDLTCRWTPGAGETFLHTNYSILKYLWR 180

QY 181 YGQDNTCEYHTVGHPSCHIPKDLALFTPYEIWIWEATNRLGSARSDVLTLDVLDVVTDP 240
 DB 181 YGQDNTCEYHTVGHPSCHIPKDLALFTPYEIWIWEATNRLGSARSDVLTLDVLDVVTDP 240
 QY 241 PPDVHVSRVGGLEDQLSVRWVSPALKDPLFQAKYQIRYVEDSVDMKVDDVSNQTSR 300
 DB 241 PPDVHVSRVGGLEDQLSVRWVSPALKDPLFQAKYQIRYVEDSVDMKVDDVSNQTSR 300
 QY 301 LAGLKPQTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSERPGGVCPRGGE 360
 DB 301 LAGLKPQTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSERPGGVCPRGGE 360
 QY 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
 DB 361 PSSGVRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 414

RESULT 6
 ID AAE00821 standard; protein; 425 AA.
 AC AAE00821;
 DT 09-SEP-2004 (revised)
 DT 02-JUL-2001 (first entry)
 XX Murine haemopoietin receptor, NR6.2 isoform.
 KW Murine; biologically active complex; haemopoietin receptor; NR6;
 KW cardiostrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
 KW differentiation; cell survival; neurotrophic activity.
 OS Mus sp.
 OS Unidentified.
 FH Key Location/Qualifiers
 FT Domain 330..334
 FT /label = WSXWS_motif
 XX WO200127157-A1.
 PD 19-APR-2001.
 XX 06-OCT-2000; 2000WO-AU001216.
 XX 08-OCT-1999; 99AU-00003327.
 PR 12-MAY-2000; 2000AU-00007489.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 PA Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
 PI Nakata Y, Hasegawa M;
 XX WPI: 2001-281978/29.
 DR N-PSDB; AAD04193.
 XX New biologically active complex comprising NR6 and cardiostrophin-like-
 cytokine, for facilitating proliferation, differentiation and/or survival
 of a cell.
 PS Claim 26; Page 81-83; 123pp; English.
 XX The present invention relates to a biologically active complex comprising
 a haemopoietin receptor, NR6 and cardiostrophin-like cytokine (CLC). The
 complex is useful in the manufacture of a medicament for the treatment
 and/or prophylaxis of a subject, as it is involved in facilitating
 proliferation, differentiation and/or survival of a cell. The complex or
 its components have neurotrophic activity. The present sequence is murine
 haemopoietin receptor, NR6.2 isoform. The NR6.2 represents the NR6 splice
 variant obtained due to alternative mRNA splicing

Revised record issued on 09-SEP-2004 : Correction to Feature Table Key


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SQ      Sequence 425 AA;
Query Match      98.9%; Score 2226.5; DB 4; Length 425;
Best Local Similarity 98.8%; Pred. No. 3.5e-184;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY      1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLQ 60
Db      1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLQ 60

QY      61 ATCSIHGDTPGATAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
Db      61 ATCSIHGDTPGATAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY      121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSCLKYLRW 180
Db      121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSCLKYLRW 180

QY      181 YGQDNTCEBYHTVGPCHSCHI PKDLALFTPYEIVWEATNRLGARSVDLTLVDLVVTTDP 240
Db      181 YGQDNTCEBYHTVGPCHSCHI PKDLALFTPYEIVWEATNRLGARSVDLTLVDLVVTTDP 240

QY      241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVDSNQTSCR 300
Db      241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVDSNQTSCR 300

QY      301 LAGLKPGTVYFVQVRCNPFYIGYKKGAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360
Db      301 LAGLKPGTVYFVQVRCNPFYIGYKKGAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360

QY      361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411
Db      361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 7
AAW59804
ID      AAW59804 standard; protein; 425 AA.
AC      AAW59804;
XX
XX
DT      26-OCT-1998 (first entry)
DE      Nucleotide sequence of the murine U4 protein.
KW      Murine; U4 protein; haematopoietin receptor superfamily;
KW      cell proliferation; immune response; antibody; cell differentiation;
KW      autoimmune disease; cancer; allergy.
OS      Mus sp.
XX
XX      WO9831811-A1.
XX
XX      23-JUL-1998.
XX
XX      15-JAN-1998; 98WO-US000334.
XX
XX      16-JAN-1997; 97US-00784863.
XX
XX      (GENY ) GENETICS INST INC.
XX
XX      Donaldson DD, Collins M, Neben T, Whitters M;
XX
XX      WPI; 1998-414109/35.
XX
XX      N-PSDB; AAV41688.
XX
XX      New nucleic acid encoding U4 haematopoietin receptor superfamily chain -
XX      PT potentially useful, e.g. for modulating cell proliferation or immune
XX      response, for treating cancer and auto-immune disease.
XX
XX      Claim 9; Page 26-27; 38pp; English.
XX
XX      This is the amino acid sequence of the murine U4 protein from the

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CC      haematopoietin receptor superfamily, used in the method of the invention
CC      for the modulation of cell proliferation, or the immune response.
CC      Transformed mammalian cells are used to produce recombinant U4 protein.
CC      The U4 protein is used to screen for specific binding agents, raise
CC      antibodies. It is also used as reagents for assays and as tissue markers
CC      for isolation of cognate ligands and receptors, and in pharmaceutical
CC      compositions which may modulate cell proliferation, cell differentiation,
CC      and the immune system (e.g. for treating immune deficiency, inherited or
CC      the result of infection, autoimmune diseases, cancer, and allergy)
XX
SQ      Sequence 425 AA;

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Query Match      98.7%; Score 2222.5; DB 2; Length 425;
Best Local Similarity 98.6%; Pred. No. 7.8e-184;
Matches 408; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY      1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLQ 60
Db      1 MPAGRPGPVAQSAARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLQ 60

QY      61 ATCSIHGDTPGATAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
Db      61 ATCSIHGDTPGATAGLYWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY      121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSCLKYLRW 180
Db      121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSCLKYLRW 180

QY      181 YGQDNTCEBYHTVGPCHSCHI PKDLALFTPYEIVWEATNRLGARSVDLTLVDLVVTTDP 240
Db      181 YGQDNTCEBYHTVGPCHSCHI PKDLALFTPYEIVWEATNRLGARSVDLTLVDLVVTTDP 240

QY      241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVDSNQTSCR 300
Db      241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVDSNQTSCR 300

QY      301 LAGLKPGTVYFVQVRCNPFYIGYKKGAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360
Db      301 LAGLKPGTVYFVQVRCNPFYIGYKKGAGIWESESHPTAASTPRSRPFGGVCBPRGGE 360

QY      361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411
Db      361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

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RESULT 8
AAW26337
ID      AAW26337 standard; protein; 425 AA.
XX
XX      AAW26337;
XX
XX      13-JAN-2000 (first entry)
XX
XX      Murine U4 haematopoietin receptor superfamily chain.
XX
XX      Murine U4 protein; haematopoietin receptor superfamily;
XX      biological activity; cytokine; cell proliferation; cell differentiation;
XX      immune stimulation; immune suppression; haematopoiesis regulation;
XX      immune disorder; immune deficiency; autoimmune disorder; allergy; cancer;
XX      myeloid cell; lymphoid cell deficiency; platelet disorder.
XX
XX      Mus sp.
XX
XX      Key      Location/Qualifiers
XX      Peptide 1..40
XX      Protein 41..383
XX      /label= Putative_signal_sequence
XX      /label= Mature_murine_U4
XX
XX      WO9953066-A1.
XX
XX      21-OCT-1999.
XX

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PF 09-APR-1999; 99WO-US007882.
 XX
 PR 10-APR-1998; 98US-00058660.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Donaldson D, Collins M, Whitters M, Neben T;
 XX
 DR WPI; 1999-611303/52.
 DR N-PSDB; AAX90752.
 XX
 PT Novel polypeptides and polynucleotides used for treatment of human
 PT diseases and disorders e.g. immune disorders or deficiencies caused by
 PT fungal, parasitic or viral infections.
 XX
 XX Claim 9; Page 31-32; 43pp; English.
 PS
 XX The present sequence is a murine U4 protein which is a member of
 CC haematopoietin receptor superfamily. The protein sequence has conserved
 CC cysteine pairs and WSXS motifs characteristic of the receptor family. It
 CC is predicted to have the following biological activities: cytokine, cell
 CC proliferation/differentiation, immune stimulating or suppressing and
 CC haematopoiesis regulating. The U4 protein can be used to treat immune
 CC disorders and deficiencies, autoimmune disorders, allergies, cancer,
 CC myeloid or lymphoid cell deficiencies and platelet disorders
 XX
 SQ Sequence 425 AA;

Query Match 98.7%; Score 2225.5; DB 2; Length 425;
 Best Local Similarity 98.6%; Pred. No. 7.8e-184;
 Matches 408; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
 QY 1 MPAGRGVPAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLQ 60
 DB 1 MPAGRGVPAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLQ 60
 QY 61 ATCSIHGDTPGAETAGLYWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGAETAGLYWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
 DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
 QY 181 YGQDNTCEEVHTVGPSCHPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDP 240
 DB 181 YGQDNTCEEVHTVGPSCHPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDP 240
 QY 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVSNQTSR 300
 DB 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVSNQTSR 300
 QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGVCPEPRGGE 360
 DB 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGVCPEPRGGE 360
 QY 361 PSSGPVRELRKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411
 DB 361 PSSGPVRELRKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 9
 AAW70862
 ID AAW70862 standard; protein; 425 AA.
 XX
 AC AAW70862;
 XX
 DT 17-MAR-1999 (first entry)
 XX
 DE Rat Zcytor5 protein.
 XX
 KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;

KW cardiac pathology; heart enlargement; Zcytor5 ligand.
 XX
 OS Rattus sp.
 XX
 PN WO9849307-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 01-MAY-1998; 98WO-US008865.
 XX
 PR 01-MAY-1997; 97US-0045287P.
 PR 01-MAY-1997; 97US-00850030.
 PR 13-FEB-1998; 98US-00023890.
 PR 13-FEB-1998; 98US-0074721P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Lok S, Preenell SR, Jelmberg AC, Gilbert T, Whitmore TE;
 PI Foster DC, Adams RL, Lehner JM;
 DR WPI; 1999-034662/03.
 XX N-PSDB; AAV70896.
 XX New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-
 PT regulating Zcytor5 natural ligands or detecting cardiostrophin-1 in blood.
 XX
 PS Claim 1; Page 75-76; 55pp; English.
 XX
 CC The present sequence represents a protein designated Zcytor5, which is a
 CC cytokinin-like receptor. Soluble Zcytor5 may be administered to down-
 CC regulate the effects of a growth and/or maintenance factor in thyroid,
 CC heart, and skeletal muscle for example to lessen the effect of
 CC cardiostrophin-1 on cardiac pathologies, so preventing heart enlargement.
 CC Zcytor5 could be used to detect cardiostrophin-1 in the blood, and to
 CC discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA
 CC or RNA can be used to determine the presence and integrity of the Zcytor5
 CC gene on chromosome 19. Antibodies and the anti-idiotypic antibody could
 CC be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand
 CC effects
 XX
 SQ Sequence 425 AA;
 Query Match 97.6%; Score 2197.5; DB 2; Length 425;
 Best Local Similarity 97.6%; Pred. No. 1.1e-181;
 Matches 404; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
 QY 1 MPAGRGVPAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLQ 60
 DB 1 MPAGRGVPAQAARRPRPLSSLSWSPLLLCVLGVPGRGSGAHTAVISPDPTLLIGSSLH 60
 QY 61 ATCSIHGDTPGAETAGLYWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGAETAGLYWTLNGRRPLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
 DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
 QY 181 YGQDNTCEEVHTVGPSCHPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDP 240
 DB 181 YGQDNTCEEVHTVGPSCHPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDP 240
 QY 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVSNQTSR 300
 DB 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDVSNQTSR 300
 QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGVCPEPRGGE 360
 DB 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASPRSERPGGVCPEPRGGE 360
 QY 361 PSSGPVRELRKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411
 DB 361 PSSGPVRELRKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 414

RESULT 10
 AAY29780
 ID AAY29780 standard; protein; 416 AA.
 XX
 AC AAY29780;
 XX
 DT 04-NOV-1999 (first entry)
 XX
 DE Mouse DNAX soluble receptor subunit 1.
 XX
 KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
 KW interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;
 KW inflammatory disorder; inflammatory response; innate immunity;
 KW morphogenic development; immunological disorder.
 XX
 OS Mus sp.
 XX
 PN WO9940195-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 05-FEB-1999; 99WO-US002600.
 XX
 PR 06-FEB-1998; 98US-0073941P.
 PR 13-MAY-1998; 98US-00078194.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Matteson JD, Mcclanahan TK, Kastelein RA;
 XX
 DR WPI; 1999-527306/44.
 DR N-PSDB; AA208862.
 XX
 PT New receptor subunits useful in the treatment inflammatory disorders.
 PS
 PS Claim 2; Page 24-25; 133pp; English.
 XX
 CC The present invention describes a composition (I) comprising DNAX
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
 CC subunit I (DSRS1) protein, which together encode a new mammalian cytokine
 CC -related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or
 CC DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRS1 is useful for
 CC screening for ligands (i.e. agonists/antagonists) from a library of
 CC compounds, which are useful for modulating the physiology or development
 CC of a cell or tissue culture e.g. inflammatory responses, innate immunity
 CC and/or morphogenic development. (R), antibodies and ligands are useful
 CC for treatment of conditions, especially immunological disorders,
 CC associated with conditions exhibiting abnormal expression of (R). (R) is
 CC useful as a phosphate labeling enzyme to label substrates, and the
 CC subunits DSRs1 and DCRS1 are useful as immunogens for generating
 CC antibodies, or as antigens for binding antibodies. Nucleic acids encoding
 CC (R) are useful for identifying related DNAs and mRNAs, and variants from
 CC other individuals or species. The present sequence represents the
 CC specifically claimed mouse DSRs1, for use in the composition of the
 CC present invention
 XX
 SQ Sequence 416 AA;
 Query Match 94.8%; Score 2134.5; DB 2; Length 416;
 Best Local Similarity 98.7%; Pred. No. 3.3e-176;
 Matches 392; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
 QY 18 RPLSLWSPLLCLVGVPRGGSGANTAVISPODPTLLIGSSLOATCSIHGDPFGATAGL 77
 DB 9 RPLSLWSPLLCLVGVPRGGSGANTAVISPODPTLLIGSSLOATCSIHGDPFGATAGL 68
 QY 78 YWTLNGRRPLPSLSRLINTSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYVGLP 137
 DB 69 YWTLNGRRPLPSLSRLINTSTLALANLNGSRQSGDNLVCHARDGSLIAGSCLYVGLP 128
 QY 138 PEKPFNISCWSRMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEYHTVGPHS 197

DB 129 PEKPFNISCWSRMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEYHTVGPHS 188
 QY 198 CHIPKDLALFTPEIWEATNRLGARSVDLTDLVDVVTTPDPDVHVSRYGGLEDQLS 257
 DB 189 CHIPKDLALFTPEIWEATNRLGARSVDLTDLVDVVTTPDPDVHVSRYGGLEDQLS 248
 QY 258 VRWVSPALKDPLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKPCTVYFVQVRCN 317
 DB 249 VRWVSPALKDPLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKPCTVYFVQVRCN 308
 QY 318 PGIYGSCKAGIWSHSHPTAASRSPRPGGGVCEPRGCGSPGVRRELKQPLGWL 377
 DB 309 PGIYGSCKAGIWSHSHPTAASRSPRPGGGVCEPRGCGSPGVRRELKQPLGWL 368
 QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411
 DB 369 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 405

RESULT 11
 AAB19589
 ID AAB19589 standard; protein; 407 AA.
 XX
 AC AAB19589;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Mouse cytokine-like factor-1.
 XX
 KW Cytokine-like factor-1; CLF-1; interleukin-B60; IL-B60; mouse; cytokine;
 KW receptor; neuron; inflammation; antiinflammatory; autoimmune disease;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 PN WO200053631-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US0006182.
 XX
 PR 11-MAR-1999; 98US-00267901.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;
 XX
 WPI; 2000-587426/55.
 XX
 CC Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
 CC polypeptides, and nucleic acids, useful in research, diagnosis and for
 CC treating inflammatory and autoimmune disorders.
 XX
 PS Claim 1; Page 21-22; 97pp; English.
 XX
 CC The present sequence is that of mouse cytokine-like factor-1 (CLF-1), a
 CC cytokine receptor family protein, which forms a complex with human
 CC interleukin-B60 (IL-B60, see AAB19586). The IL-B60/CLF-1 cytokine serves
 CC as a key physiological factor in motor neuron development and
 CC regeneration. A claimed soluble complex comprises at least 6 amino acids
 CC of mature IL-60B, at least 6 amino acids of mature CLF-1 or at least 6
 CC amino acids of mature CNTF-R. A claimed method of modulating the
 CC physiology or development of a cell or tissue culture cell involves
 CC contacting the cell with an agonist or antagonist of a complex comprising
 CC IL-60B and CLF-1 or CNTF-R. A claimed method of screening for a receptor
 CC which binds the complex involves contacting the complex with a cell
 CC expressing the receptor, to form a detectable interaction resulting in a
 CC physiological response in the cell
 XX
 SQ Sequence 407 AA;

Query Match 94.1%; Score 2119; DB 3; Length 407;

Best Local Similarity 98.5%; Pred. No. 7e-175;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;
QY 18 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 77
DB 1 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 60
QY 78 YWTLNGRLPSLSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 137
DB 61 YWTLNGRLPS-LSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 119
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 197
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 179
QY 198 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 257
DB 180 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 239
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 317
DB 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 299
QY 318 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 377
DB 300 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLP 411
DB 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

Best Local Similarity 98.5%; Pred. No. 7e-175;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;
QY 18 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 77
DB 1 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 60
QY 78 YWTLNGRLPSLSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 137
DB 61 YWTLNGRLPS-LSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 119
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 197
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 179
QY 198 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 257
DB 180 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 239
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 317
DB 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 299
QY 318 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 377
DB 300 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLP 411
DB 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

RESULT 12
AAB36648
ID AAB36648 standard; protein; 407 AA.
XX AAB36648;
AC
DT 13-MAR-2001 (first entry)
XX
DE Mouse cytokine receptor subunit NR6 protein SEQ ID NO:5.
XX
KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW modulating cell proliferation; diagnosis; detection; drug screening;
KW immunological disorder.
XX
OS Mus sp.
PN WO200073451-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US014867.
XX
PR 01-JUN-1999; 99US-00322913.
XX
PA (SCHE) SCHERING CORP.
XX
PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
XX
XX WPI; 2001-061536/07.

RESULT 12
AAB36648
ID AAB36648 standard; protein; 407 AA.
XX AAB36648;
AC
DT 13-MAR-2001 (first entry)
XX
DE Mouse cytokine receptor subunit NR6 protein SEQ ID NO:5.
XX
KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW modulating cell proliferation; diagnosis; detection; drug screening;
KW immunological disorder.
XX
OS Mus sp.
PN WO200073451-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US014867.
XX
PR 01-JUN-1999; 99US-00322913.
XX
PA (SCHE) SCHERING CORP.
XX
PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
XX
XX WPI; 2001-061536/07.

Novel composition comprising DNAX cytokine receptor subunit polypeptide
useful for regulating immune system function and for treating
immunological disorders.
XX
XX Disclosure; Page 13-15; 93pp; English.
XX
XX The present invention describes a composition (I) comprising a
XX recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The
XX DCRS2 polypeptide is useful for binding ligands and for preparing cell
XX antibodies. The DCRS2 polypeptide is also useful for modulating cell
XX proliferation, for diagnostic and therapeutic applications, for detecting

Novel composition comprising DNAX cytokine receptor subunit polypeptide
useful for regulating immune system function and for treating
immunological disorders.
XX
XX Disclosure; Page 13-15; 93pp; English.
XX
XX The present invention describes a composition (I) comprising a
XX recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The
XX DCRS2 polypeptide is useful for binding ligands and for preparing cell
XX antibodies. The DCRS2 polypeptide is also useful for modulating cell
XX proliferation, for diagnostic and therapeutic applications, for detecting

presence of their ligands and in drug screening assays. It is also useful
for treating conditions such as immunological disorders. The present
sequence represents a cytokine receptor subunit protein which is given in
an alignment of various cytokine receptor subunits in the exemplification
of the present invention
SQ Sequence 407 AA;

presence of their ligands and in drug screening assays. It is also useful
for treating conditions such as immunological disorders. The present
sequence represents a cytokine receptor subunit protein which is given in
an alignment of various cytokine receptor subunits in the exemplification
of the present invention
SQ Sequence 407 AA;

Query Match 94.1%; Score 2119; DB 4; Length 407;
Best Local Similarity 98.5%; Pred. No. 7e-175;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

Query Match 98.5%; Pred. No. 7e-175;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

QY 18 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 77
DB 1 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 60
QY 78 YWTLNGRLPSLSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 137
DB 61 YWTLNGRLPS-LSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 119
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 197
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 179
QY 198 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 257
DB 180 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 239
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 317
DB 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 299
QY 318 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 377
DB 300 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLP 411
DB 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

QY 18 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 77
DB 1 RPLSLWSPFLLCVIGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTTPGATAGL 60
QY 78 YWTLNGRLPSLSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 137
DB 61 YWTLNGRLPS-LSRLNTSTLTALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 119
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 197
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLWYQDNTCEBYHTVGPHS 179
QY 198 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 257
DB 180 CHIPKDALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDVHVS RVGGLEDQLS 239
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 317
DB 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLAGLKP GTVYFVQVRCN 299
QY 318 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 377
DB 300 PFGYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGEPSSGPVRRRELKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLP 411
DB 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

RESULT 13
ADC07180
ID ADC07180 standard; protein; 407 AA.
XX ADC07180;
AC
DT 18-DEC-2003 (first entry)
XX
DE Mouse cytokine receptor subunit NR7.
XX
KW DNAX cytokine receptor subunit 2; DCRS2; cell physiology;
KW cell development; cell culture; interferon detection;
KW immune system disorder; NR6; mouse.
XX
OS Mus sp.
PN US2003082734-A1.
XX
PD 01-MAY-2003.
XX
PF 18-SEP-2002; 2002US-00247463.
XX
PR 01-JUN-1999; 99US-0137159P.
PR 31-MAY-2000; 2000US-00588113.
XX
PA (DOWL/) DOWLING L M.
PA (TIMA/) TIMANS J C.
PA (GORM/) GORMAN D M.
PA (KAST/) KASTELEIN R A.
PA (BAZA/) BAZAN J F.
XX
PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;

RESULT 13
ADC07180
ID ADC07180 standard; protein; 407 AA.
XX ADC07180;
AC
DT 18-DEC-2003 (first entry)
XX
DE Mouse cytokine receptor subunit NR7.
XX
KW DNAX cytokine receptor subunit 2; DCRS2; cell physiology;
KW cell development; cell culture; interferon detection;
KW immune system disorder; NR6; mouse.
XX
OS Mus sp.
PN US2003082734-A1.
XX
PD 01-MAY-2003.
XX
PF 18-SEP-2002; 2002US-00247463.
XX
PR 01-JUN-1999; 99US-0137159P.
PR 31-MAY-2000; 2000US-00588113.
XX
PA (DOWL/) DOWLING L M.
PA (TIMA/) TIMANS J C.
PA (GORM/) GORMAN D M.
PA (KAST/) KASTELEIN R A.
PA (BAZA/) BAZAN J F.
XX
PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;

XX WPI; 2003-730048/69.
XX Composition potentially useful for treating immunological disorders,
XX comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a
PT natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2
PT sequence.
XX
XX Disclosure; SEQ ID NO 5; 41pp; English.
XX
XX The invention describes a composition of matter (I) comprising a
CC substantially pure or recombinant DNAX cytokine receptor subunit 2
CC (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein
CC comprising a DCRS2 sequence. A composition of matter comprises: a
CC substantially pure or recombinant DCRS2 polypeptide comprising at least
CC three distinct nonoverlapping segments of at least four amino acids
CC identical to segments of a fully defined 384 amino acid sequence (S1),
CC given in the specification; a substantially pure or recombinant DCRS2,
CC polypeptide comprising at least two distinct nonoverlapping segments of
CC at least five amino acids identical to segments of S1; a natural sequence
CC DCRS2 comprising S1; or a fusion polypeptide comprising a DCRS2 sequence.
CC An agonist or antagonist of a mammalian DCRS2 is useful for modulating
CC physiology or development of a cell or cell culture. Antibodies to a
CC DCRS2 can be used for quantitative detection of interferon. The DCRS2
CC polypeptides and nucleic acids and their binding agents are potentially
CC useful in treating and diagnosing disease, especially disease associated
CC with the immune system. This is the amino acid sequence of mouse cytokine
CC receptor subunit NR6 used in a comparison with DCRS2.
XX
XX Sequence 407 AA;
SQ
Query Match 94.1%; Score 2119; DB 7; Length 407;
Best Local Similarity 98.5%; Pred. No. 7e-175; 0; Indels 4; Gaps 2;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;
QY 18 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77
DB 1 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60
QY 78 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137
DB 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGODNTCEBYHTVGPHS 197
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGODNTCEBYHTVGPHS 179
QY 198 CHIPKDHALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 257
DB 180 CHIPKDHALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 239
QY 258 VRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKPVTYFVQVRCN 317
DB 240 VRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKPVTYFVQVRCN 299
QY 318 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 377
DB 300 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 411
DB 360 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 396
RESULT 14
ADT90845
ID ADT90845 standard; protein; 407 AA.
XX
XX ADT90845;
XX
XX 16-DEC-2004 (first entry)
XX
XX Mouse cytokine-like factor 1 (CLF-1).

XX Interleukin; IL-B60; cytokine-like factor 1; CLF-1; CNTF-R;
KW CNTF-receptor; inflammatory condition; autoimmune disorder; mouse.
XX
XX Mus sp.
XX
XX US2004192891-A1.
XX 30-SEP-2004.
XX
XX 11-FEB-2004; 2004US-00778002.
XX
XX 11-MAR-1999; 99US-0124319P.
XX 09-MAR-2000; 2000US-00521335.
XX (SCHE) SCHERING CORP.
XX
XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;
PI WPI; 2004-698788/68.
DR GENBANK; NM_004750.
DR
XX Novel mammalian cytokines, useful for producing antigen-antibody complex,
PT treating conditions associated with abnormal physiology or development,
PT including inflammatory conditions and/or autoimmune disorders.
XX
XX Claim 1; SEQ ID NO 13; 41pp; English.
XX
XX The invention relates to a complex comprising interleukin (IL)-B60,
CC cytokine-like factor 1 (CLF-1) (partner sequence of IL-B60) and CNTF-R
CC (CNTF-receptor). The complex is useful for producing an antigen-antibody
CC complex, useful for treating conditions associated with abnormal
CC physiology or development, including inflammatory conditions and/or
CC autoimmune disorders and for generating antibodies which is useful in
CC diagnostic applications. The present sequence is mouse cytokine-like
CC factor 1 (CLF-1).
XX
XX Sequence 407 AA;
Query Match 94.1%; Score 2119; DB 8; Length 407;
Best Local Similarity 98.5%; Pred. No. 7e-175; 0; Indels 4; Gaps 2;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;
QY 18 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77
DB 1 RPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60
QY 78 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137
DB 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119
QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGODNTCEBYHTVGPHS 197
DB 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGODNTCEBYHTVGPHS 179
QY 198 CHIPKDHALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 257
DB 180 CHIPKDHALFTPEYIWEATNRLGARSVDLTLDVLDVTTDPPDPPDVHVSRYVGGLEDQLS 239
QY 258 VRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKPVTYFVQVRCN 317
DB 240 VRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLRLAGLKPVTYFVQVRCN 299
QY 318 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 377
DB 300 PFGIYGSKKAGIWESEWSHPTAASRPRSGPGGGVCEPRGGEPSGPVRRRLKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 411
DB 360 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 396
RESULT 15

ADT61033
ID ADT61033 standard; protein; 407 AA.
XX AC ADT61033;
XX DT 16-DEC-2004 (first entry)
XX DE Mouse cytokine-like factor 1 (CLF-1).
XX KW Cytokine; interleukin-B60; IL-B60; cell physiology; immune system;
KW haematopoietic cell; immune disorder; T cell immune deficiency;
KW chronic inflammation; tissue rejection; cardiovascular condition;
KW neurophysiological condition; mouse; cytokine-like factor 1; CLF-1.
XX OS Mus sp.
XX PN US6800460-B1.
XX PD 05-OCT-2004.
XX PF 09-MAR-2000; 2000US-00521335.
XX PR 11-MAR-1999; 99US-0124319P.
XX PA (SCHE) SCHERING CORP.
XX PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;
XX WPI; 2004-697202/68.
XX DR New isolated or non-human host cells transfected with expression vectors
XX PT having nucleic acids encoding cytokines, useful in treating immune
XX PT disorders, cardiovascular or neurophysiological conditions.
XX PS Disclosure; SEQ ID NO 13; 37pp; English.
XX CC The invention relates to mammalian interleukin-B60 (IL-B60). The
CC invention also provides a method of producing a soluble complex
CC comprising the mature protein portions of IL-B60 and CLF-1 polypeptides.
CC The methods and compositions of the present invention are useful in
CC controlling biology and physiology of mammalian cells, such as cells of a
CC mammalian immune system, and in particular for regulating activation,
CC development, differentiation and function of various cell types,
CC including haematopoietic cells. They are specifically useful in treating
CC abnormal medical conditions, including immune disorders, such as T cell
CC immune deficiency, chronic inflammation or tissue rejection, or in
CC cardiovascular or neurophysiological conditions. The present sequence is
CC the mouse cytokine-like factor 1 (CLF-1).

Search completed: April 11, 2006, 02:09:56
Job time : 113.845 secs

Query Match 94.1%; Score 2119; DB 8; Length 407;
Best Local Similarity 98.5%; Pred. No. 7e-175;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;
QY 18 RPLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLQATCSIHGDTFGATAEGL 77
DB 1 RPLSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLQATCSIHGDTFGATAEGL 60
QY 78 YWTINGRRRLPSELRLINTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 137
DB 61 YWTINGRRRLPS-LSRLINTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLYVGLP 119
QY 138 PERPFNISCWRNMKDLTCRWTPGAGHGETFLHNTNYSKYLKRWYGDNTCEEYHTVGPHS 197
DB 120 PERPFNISCWRNMKDLTCRWTPGAGHGETFLHNTNYSKYLKRWYGDNTCEEYHTVGPHS 179
QY 198 CHIPKDLALFTPEIWEATNRLGARSDDLTLDLVDVVTTPPPDVHVSRVGGLDQLS 257
DB 180 CHIPKDLALFTPEIWEATNRLGARSDDLTLDLVDVVTTPPPDVHVSRVGGLDQLS 239
QY 258 VRWVSPPALXDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAGLKGTVYFVQVRCN 317
XX
XX Sequence 407 AA;

Db 240 VRWVSPPALXDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAGLKGTVYFVQVRCN 299
QY 318 PFGIYGSKKAGIWSWSHPTAASTPRSRPGRGGVCEPRGGEPSGVPVRRRLKQFLGWL 377
Db 300 PFGIYGSKKAGIWSWSHPTAASTPRSRPGRGGVCEPRGGEPSGVPVRRRLKQFLGWL 359
QY 378 KKHAYCSNLSPELYDOWBAWMOKSHKTRNQ---VLPA 411
Db 360 KKHAYCSNLSPELYDOWBAWMOKSHKTRNQDEGILPS 396

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: April 11, 2006, 02:10:19 ; Search time 20.6664 Seconds
(without alignments)
1922.808 Million cell updates/sec
Title: US-09-037-657-13
Perfect score: 2251
Sequence: 1 MPAGRPGVQAQARRPRPL.....WRAMQKSHKTRNQVLPAKL 413
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Match Length	Description
1	331	14.7	288 2 B59405 prolactin receptor
2	331	14.7	376 2 A59405 prolactin receptor
3	331	14.7	622 2 A40144 prolactin receptor
4	329	14.6	918 2 A36337 membrane glycoprot
5	319.5	14.2	917 2 I49699 glycoprotein 130 -
6	317.5	14.1	918 2 A44257 interleukin-6 sign
7	314	13.9	830 2 I50455 prolactin receptor
8	312	13.9	310 2 A29884 prolactin receptor
9	312	13.9	412 2 A41070 prolactin receptor
10	312	13.9	610 2 A34631 prolactin receptor
11	312	13.9	610 2 A36116 prolactin receptor
12	307.5	13.7	292 2 I77525 prolactin receptor
13	307.5	13.7	303 2 I77524 prolactin receptor
14	307.5	13.7	608 2 I53269 prolactin receptor
15	307.5	13.7	616 2 A30304 prolactin receptor
16	306	13.6	831 2 JQ1655 prolactin receptor
17	302.5	13.4	581 2 I45971 prolactin receptor
18	261.5	11.6	630 2 I51086 prolactin receptor
19	254.5	11.3	771 2 B38252 granulocyte colony
20	254.5	11.3	783 2 JH0329 granulocyte colony
21	254.5	11.3	863 2 C38252 granulocyte colony
22	252.5	11.2	837 2 A34898 granulocyte colony
23	234	10.4	372 2 I58141 ciliary neurotroph
24	220.5	9.8	372 1 UHUCN ciliary neurotroph
25	209.5	9.3	422 2 I37891 interleukin-11 rec
26	208.5	9.3	432 2 I48343 interleukin-11 rec
27	208	9.2	362 2 S60614 growth promoting a
28	203.5	9.0	460 2 JL0145 interleukin-6 rece
29	200.5	8.9	468 1 A41242 interleukin-6 rece

ALIGNMENTS

RESULT 1

B59405 prolactin receptor short form Sib precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: B59405; B49400

R:Hu, Z.Z.; Meng, J.; Dufau, M.L.

J: Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin recep

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: B59405

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU1>

A:Cross-references: UNIPROT:Q96P36; UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1

R:Hu, Z.Z.

Submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: B49400

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU2>

A:Cross-references: UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1

C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor

ta-casein gene promoter activation, with S1b more effective than S1a. However, their li

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:I20315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-288/Product: prolactin receptor, short form Sib #status predicted <WAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 14.7%; Score 331; DB 2; Length 288;

Best Local Similarity 37.5%; Pred. No. 2,7e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAAGCLVYVG-LPPKPPNISCWNRNMKDLTCRTPGAGHGTFLHTNYSLKYLRYGQD 184

Db 15 LFLNTCLLGLPPCKPEIFKCRSPNKETFTWRRPDTGG--LPNTYSLTYHREGTELM 72

QY 185 NTCERYHTVGHSHCHIPKD-LALFTPEIYIWWATNRLGARSADVLTLDVLDVTTDPPPD 243

Db 73 HECPDYITGGPNRSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELVDVYVTVQPPPLE 132

QY 244 VHVSRVGGLEDLSVRVW--SPALKDF--LFAQKYQIRYRVSDVDMKKVDDVSNQTS 298

Db 133 LAV-EVKQPEDRPKPLWIKNSPPTLIDLTGHTFTLLYEIRLKPKEAWE-IHFACQOTE 190

QY 299 CRLAGLKPGTVYFVQVRCPNPFPGIYGGKKAGIWSWSHPTAATP 342

prolactin receptor
interleukin-6 rece
MPL-K protein prec
MPL-P protein prec
leptin receptor, s
leptin receptor, s
leptin receptor, s
leptin receptor, s
leptin receptor, s
hematopoietic grow
leukemia inhibitor
leptin receptor, O
proto-oncogene - m
differentiation-st
leptin receptor, i

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 2

A59405

prolactin receptor short form Sla precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: A59405

R:Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin receptor

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: A59405

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU>

A:Cross-references: UNIPROT:Q96P35; UNIPARC:UPI000006E673; GB:AF214012.1

R:Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: A49400

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU>

A:Cross-references: UNIPARC:UPI000006E673; GB:AF214012.1

C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor

eta-casein gene promoter activation, with sla less effective than S1b. However, their li

ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: Sp13.3-Sp13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-376/Product: prolactin receptor, short form Sla #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7%; Score 331; DB 2; Length 376;

Best Local Similarity 37.5%; Pred. No. 3.7e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLYVG-LPPEKPFNISCWSRNKDLTCRWTFGAHGETFLHTNYSLKYLRYGQD 184

Db 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETTCWWRPGTDG--LPTNYSLYTHREGETLM 72

QY 185 NTCEEYHTVGPCHPKD-LALFTPYEIVWEATNRLGARSVDLTLVDLVDVTTDPPPD 243

Db 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQSGSFDELVDVTVIIVQDPPLLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVSDVMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGNTWLLYELRLKPEKAAWE-IHFAGQOTE 190

QY 299 CRLAGLKPQTVYVQVRCNPFGLYGSKKAGINSEWSHPTAASP 342

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

Query Match 14.7%; Score 331; DB 2; Length 376;

Best Local Similarity 37.5%; Pred. No. 3.7e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLYVG-LPPEKPFNISCWSRNKDLTCRWTFGAHGETFLHTNYSLKYLRYGQD 184

Db 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETTCWWRPGTDG--LPTNYSLYTHREGETLM 72

QY 185 NTCEEYHTVGPCHPKD-LALFTPYEIVWEATNRLGARSVDLTLVDLVDVTTDPPPD 243

Db 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQSGSFDELVDVTVIIVQDPPLLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVSDVMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGNTWLLYELRLKPEKAAWE-IHFAGQOTE 190

QY 299 CRLAGLKPQTVYVQVRCNPFGLYGSKKAGINSEWSHPTAASP 342

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 3

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C:Accession: A40144; A57018

R:Boutin, J.M.; Eder, M.; Shiota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.;

Mol. Endocrinol. 3, 1455-1461, 1989

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human he

A:Reference number: A40144; MUID:90114212; PMID:2558309

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BOU>

A:Cross-references: UNIPROT:P16471; UNIPARC:UPI0000122234; GB:M31661; NID:9190361; PIDN:

R:Fuh, G.; Wells, J.A.

J. Biol. Chem. 270, 13133-13137, 1995

A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li

A:Reference number: A57018; MUID:95286597; PMID:7768908

A:Accession: A57018

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 25-228, 'AW' <RES>

A:Cross-references: UNIPARC:UPI000006D208; GB:S78505; NID:999114; PIDN:AAB34470.1; PID:

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: Sp13.3-Sp13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-622/Product: prolactin receptor, long form #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.7%; Score 331; DB 2; Length 622;

Best Local Similarity 37.5%; Pred. No. 7.1e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLYVG-LPPEKPFNISCWSRNKDLTCRWTFGAHGETFLHTNYSLKYLRYGQD 184

Db 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETTCWWRPGTDG--LPTNYSLYTHREGETLM 72

QY 185 NTCEEYHTVGPCHPKD-LALFTPYEIVWEATNRLGARSVDLTLVDLVDVTTDPPPD 243

Db 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQSGSFDELVDVTVIIVQDPPLLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVSDVMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGNTWLLYELRLKPEKAAWE-IHFAGQOTE 190

QY 299 CRLAGLKPQTVYVQVRCNPFGLYGSKKAGINSEWSHPTAASP 342

Db 191 FKILSLHPGQKYLQVQRCKP-----DHGYWSAMSPATFIQIP 227

RESULT 4

A36337

membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)

C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C:Accession: A36337

R:Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Cell 63, 1149-1157, 1990

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A:Reference number: A36337; MUID:91084844; PMID:2261637

A:Accession: A36337

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <HIB>

A:Cross-references: UNIPROT:P40189; UNIPARC:UPI0000046B12; GB:M57230; NID:9186353; PIDN:

C:Genetics:

A:Gene: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694

A:Map position: 5q11-5q11

C:Keywords: glycoprotein; membrane protein

F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 14.6%; Score 329; DB 2; Length 918;

Best Local Similarity 28.6%; Pred. No. 1.6e-17;

Matches 89; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISPDPTLLIGSSLOATCSIHG---DTPGATAGLWTNLRPLSPSELSRLNTSTLALA 102

Db 31 ISPESPVQLHSNFTAVCVLKERCMDFYHNANYIVKTNHFTIPKEQYTIINRTASSVT 90

QY 103 LANLNGSRQSGDNLVCHARDGSLAGSLYGLPPEKPFNISCWSRNKMDLTCRWTPGA 162


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Db 91 FTDIASINLTQCNILTFGLQEQNVYGITIISGLPPEKPKNLSCIVNEGKKMCEWDGGR 150
QY 163 HGETFLHTNYSKYLKWYQDMNTCBEYHTVGVPHSCHIPKDLALFTPYEITWVATNRLGS 222
Db 151 --ETHLETNFTLASEWATHKFAACKAKRDT--PTSCVDYSTVYFVNIEVWEAENALGK 206
QY 223 ARSDVLTLDVLDVTTDPPDVHVSRRVGGLEDQLSVRVSPPPALDKFLFOAKYQIIRYVE 282
Db 207 VTSDDHINFDPVYKVPKPNHLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIOYRTK 264
QY 283 DSDVMKWV---DDVSNQTSCLAGLPGTVYFVQVRCNPGIYVSGKAGIWSWSHPTAA 339
Db 265 DASTWQIPEPTASTRSSFTVQDLKPFTYEVFRIR-----WKEDGKGWSDWSEASG 319
QY 340 STPRSERP 347
Db 320 IT-YEDRP 326

RESULT 5
I49699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I49699; I48370
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:92291532; PMID:1602143
A:Accession: I49699
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: UNIPROT:Q00560; UNIPARC:UPI000002845A; GB:M83336; NID:G193591; PIDN:
A:Accession: I48370
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RE2>
A:Cross-references: UNIPARC:UPI000002845A; EMBL:X62646; NID:G840816; PIDN:CAA44515.1; PI
C:Genetics:
A:Gene: gp130
C:Keywords: Glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 14.2%; Score 319.5; DB 2; Length 917;
Best Local Similarity 29.6%; Pred. No. 9e-17;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 46 ISPDPTLLIGSSLOATCSIHG---DTPGATAGLYWTILNGRRRLPSELRLNTSTLALA 102
Db 31 IYPERPVVQSGNFTATCVLKEACLOHYVYNASIIYVWKTNHAAPREQVTVINRTTSSVT 90
QY 103 LANLNGSROQSDNLVCHARDGSLAGSCLYVGLPEKPFNISCWRNNKMDLTCRWTPGA 162
Db 91 FTDVVLPSVQLTCNIIISFGQIEQNVYGVMTLSGFPDPDKPTNLTLCIVNEGKNMLCQWDPR 150
QY 163 HGETFLHTNYSKYLKWYQDMNTCBEYHTVGVPHSCHIPKDLALFTPYEITWVATNRLG 221
Db 151 --ETYLETNYTLKSE--WATEKFPDCQKHGT---SCWVSYMTPTYYVNVIEVWEAENALG 203
QY 222 SARSDVLTLDVLDVTTDPPDVHVSRRVGGLEDQLSVRVSPPPALDKFLFOAKYQIIRYV 281
Db 204 KYVSESINFDPVDKVPKTPPNLNVSVNSELSILKLSVSSGL--GGILLDKSDIOYRT 261
QY 282 EDSVDMKWV---DDVSNQTSCLAGLPGTVYFVQVRCNPGIYVSGKAGIWSWSHPTA 338
Db 262 KDASTWQIPEPTASTRSSFTVQDLKPFTYEVFRIR-----SIKDSGK-GYNSDWSEAS 316
QY 339 AST--PRSERP 347
Db 317 GTTYEDRPSRP 327
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RESULT 6

```
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.B.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin
A:Reference number: A44257; MUID:93052397; PMID:1427893
A:Accession: A44257
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBI:P118488)
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 14.1%; Score 317.5; DB 2; Length 918;
Best Local Similarity 29.8%; Pred. No. 1.3e-16;
Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;

QY 46 ISPDPTLLIGSSLOATCSIHG---DTPGATAGLYWTILNGRRRLPSELRLNTSTLALA 102
Db 31 IYPERPVVQSGNFTATCVLKECLQVYSVNATYIYVWKTNHAAPKEQVTVINRTTASSVT 90
QY 103 LANLNGSROQSDNLVCHARDGSLAGSCLYVGLPEKPFNISCWRNNKMDLTCRWTPGA 162
Db 91 FTDVVFQNVQLTCNIIISFGQIEQNVYGITILSGYPPDIPTNLSCIVNEGKNMLCQWDPR 150
QY 163 HGETFLHTNYSKYLKWYQDMNTCBEYHTVGVPHSCHIPKDLALFTPYEITWVATNRLG 221
Db 151 --ETYLETNYTLKSE--WATEKFPDCRTRKH--GTSSCMGYPYIYVNVIEVWEAENALG 204
QY 222 SARSDVLTLDVLDVTTDPPDVHVSRRVGGLEDQLSVRVSPPPALDKFLFOAKYQIIRYV 281
Db 205 NVYSSEINFDPVDKVPKPPHNLNVSVNSELSILKLANVNSGL--DSILRLKSDIOYRT 262
QY 282 EDSVDMKWV---DDVSNQTSCLAGLPGTVYFVQVRCNPGIYVSGKAGIWSWSHPTA 338
Db 263 KDASTWQIPEPTASTRSSFTVQDLKPFTYEVFRIR-----SIKENGK-GYNSDWSE-EA 316
QY 339 ASTPRSERP 347
Db 317 SGTTYEDRP 325

RESULT 7
I50455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267; PMID:7516866
A:Accession: I50455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:G466381; PI
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 13.9%; Score 314; DB 2; Length 830;
Best Local Similarity 37.1%; Pred. No. 2.1e-16;
Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;

QY 137 PPEKPFNISCWRNNKMDLTCRWTPGAHGTFLH--TNYSILKYLKWYQDMTCBEYHTVGP 195
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Db 231 PPEKPTIIKCRPEKETFTCWKPGSDGG---HPTNYTLLYSKEGEERYVECPDYKTAGP 287
QY 196 HSCHI-PKDALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPDV--HVS RVGGL 252
Db 288 NSCYFDKHTSWTYNTIVKATNEIGNSVDPLYVDVYIYVQTDPVNVNLTLELKKTVNR 347
QY 253 EDQLSVRVWSPPALKDF---LFOAKYQIRYRVEDSVDMKVDVDSNQTSRLAGLKPGRV 309
Db 348 KPYLVLTW-SPPLADVRSGMLTLDYELRLKPEAEWETI-FVGQOYHKMFSLNPGKK 405
QY 310 YFVQVRCNPFYIGSKKAGIWEWS 334
Db 406 YIVQIHCKP-----DHGGSWSEWS 424

RESULT 8
A29884
prolactin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A29884
R:Boutin, J.M.; Jolicœur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A:Reference number: A29884; PMID:88165059; PMID:2832068
A:Accession: A29884
A:Molecule type: mRNA
A:Residues: 1-310 <BOU>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19A; GB:M19304; NID:g206364; PIDN:
C:Keywords: transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-310/Product: prolactin receptor #status predicted <MAT>
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 312; DB 2; Length 310;
Best Local Similarity 35.4%; Pred. No. 8.8e-17;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SILAGSLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTNYSLKYLKRWYGD 184
Db 15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWNPETDGG--LPTNYSLTYSKE--GEK 65

QY 185 NT--CEEYHTVGPCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPP 241
Db 66 TTVECPDYKTSGPSNCFPSKQVTSIWKIYIITVNATNQMGSSSDPLYVDVTVIVEPEPP 125

QY 242 PDVHVS RVGGLDQLSVRWV--SPPALKDF---LFOAKYQIRYRVEDSVDMKVDVDSNQ 296
Db 126 RNLT-L-EVKQLDKKTYLWVKSPTITDVKTGWFTMEYIRLKPBEAEWE-IHFTGHQ 183

QY 297 TSCRLAGLKPGRVYFVQVRCNPFYIGSKKAGIWEWSHPTAASP 342
Db 184 TQPKVFDLPQKYLVTQTRCKP-----DHGYWSRWSQESSVEMP 222

Query Match 13.9%; Score 312; DB 2; Length 310;
Best Local Similarity 35.4%; Pred. No. 8.8e-17;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SILAGSLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTNYSLKYLKRWYGD 184
Db 15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWNPETDGG--LPTNYSLTYSKE--GEK 65

QY 185 NT--CEEYHTVGPCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPP 241
Db 66 TTVECPDYKTSGPSNCFPSKQVTSIWKIYIITVNATNQMGSSSDPLYVDVTVIVEPEPP 125

QY 242 PDVHVS RVGGLDQLSVRWV--SPPALKDF---LFOAKYQIRYRVEDSVDMKVDVDSNQ 296
Db 126 RNLT-L-EVKQLDKKTYLWVKSPTITDVKTGWFTMEYIRLKPBEAEWE-IHFTGHQ 183

QY 297 TSCRLAGLKPGRVYFVQVRCNPFYIGSKKAGIWEWSHPTAASP 342
Db 184 TQPKVFDLPQKYLVTQTRCKP-----DHGYWSRWSQESSVEMP 222

RESULT 9
A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41070; I55417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolact
A:Reference number: A41070; PMID:92041834; PMID:1718958
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN:
R:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor

A:Reference number: I55417; PMID:95014432; PMID:7929319
A:Accession: I55417
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-412 <REG>
A:Cross-references: UNIPARC:UPI000002B19B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PI:
A:Experimental source: Nb2-11C cell line
C:Keywords: transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 312; DB 2; Length 412;
Best Local Similarity 35.4%; Pred. No. 1.3e-16;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SILAGSLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTNYSLKYLKRWYGD 184
Db 15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWNPETDGG--LPTNYSLTYSKE--GEK 65

QY 185 NT--CEEYHTVGPCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPP 241
Db 66 TTVECPDYKTSGPSNCFPSKQVTSIWKIYIITVNATNQMGSSSDPLYVDVTVIVEPEPP 125

QY 242 PDVHVS RVGGLDQLSVRWV--SPPALKDF---LFOAKYQIRYRVEDSVDMKVDVDSNQ 296
Db 126 RNLT-L-EVKQLDKKTYLWVKSPTITDVKTGWFTMEYIRLKPBEAEWE-IHFTGHQ 183

QY 297 TSCRLAGLKPGRVYFVQVRCNPFYIGSKKAGIWEWSHPTAASP 342
Db 184 TQPKVFDLPQKYLVTQTRCKP-----DHGYWSRWSQESSVEMP 222

RESULT 10
A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C:Accession: A34631
R:Zhang, R.; Buczek, E.; Tsai-Morris, C.H.; Hu, Z.-Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cdna
A:Reference number: A34631; PMID:90241201; PMID:2159291
A:Accession: A34631
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <ZHA>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170B1; GB:M34083; NID:g205122; PIDN:
A>Note: the authors translated the codon GAG for residue 533 as Gly
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 312; DB 2; Length 610;
Best Local Similarity 35.4%; Pred. No. 2.1e-16;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SILAGSLVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTNYSLKYLKRWYGD 184
Db 15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWNPETDGG--LPTNYSLTYSKE--GEK 65

QY 185 NT--CEEYHTVGPCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPP 241
Db 66 TTVECPDYKTSGPSNCFPSKQVTSIWKIYIITVNATNQMGSSSDPLYVDVTVIVEPEPP 125

QY 242 PDVHVS RVGGLDQLSVRWV--SPPALKDF---LFOAKYQIRYRVEDSVDMKVDVDSNQ 296
Db 126 RNLT-L-EVKQLDKKTYLWVKSPTITDVKTGWFTMEYIRLKPBEAEWE-IHFTGHQ 183

QY 297 TSCRLAGLKPGRVYFVQVRCNPFYIGSKKAGIWEWSHPTAASP 342
Db 184 TQPKVFDLPQKYLVTQTRCKP-----DHGYWSRWSQESSVEMP 222

RESULT 11
A36116
prolactin receptor 2 precursor - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36116
R;Shioto, M.; Banville, D.; Ali, S.; Jolicœur, C.; Boutin, J.M.; Ederly, M.; Djiane, J.
Mol. Endocrinol. 4, 1136-1143, 1990
A;Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A;Reference number: A36116; MUID:91155946; PMID:2293022
A;Accession: A36116
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-610 <SHI>
A;Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170ADB; GB:M57668; NID:g206366; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 312; DB 2; Length 610;
Best Local Similarity 35.4%; Pred. No. 2.1e-16;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SILAGSLYGLPPEKPFNISCWSRNKMLTCTWTPGAHGETFLHTNYSKYKLRWYQD 184
DB 15 SLKQGS-----PPGKPEIHKCRSPDKETFTCWNPFGTDGG--LPTNYSLYTSKE--GEK 65

QY 185 NT--CEEYHTVGHPSCHIPKD-LALPTPEIWEATNRLGARSDDLTLVDLVVTTDPP 241
DB 66 TTYECPDYKTSKSPNCSFFSKQYTSIWKIYIITVNATNMGSSSDPLYVDVTVIVBPEPP 125

QY 242 PDVHVSRLVGLPPEKPFNISCWSRNKMLTCTWTPGAHGETFLHTNYSKYKLRWYQD 296
DB 126 RNLTL-EVKQLKDKKTYLWYKWSPTITDVKTCWFTWEYIRLKPBAEWE-IHFTGHQ 183

QY 297 TSCRLAGLPGTVYFVQVRCNPPFGIYGSKKAGIWSWSHPTAATP 342
DB 184 TQPKVFDLYPGQKYLQVTRCKP-----DHGYWSRWSQESSVEMP 222

RESULT 12
I77525
prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I77525
R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the prolactin receptor in mouse liver.
A;Reference number: I57699; MUID:89261824; PMID:2725531
A;Accession: I77525
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-292 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B198; GB:M22959; NID:g200481; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 307.5; DB 2; Length 292;
Best Local Similarity 32.8%; Pred. No. 1.8e-16;
Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

QY 90 LSRLMTSTLALANLNGSRQSGDNLVCHARDGSIAGSLYGLPPEKPFNISCWSR 149
DB 1 MSSALAYMLLVLSISLNG--QS-----PPGKPEIHKCRSP 34

QY 150 NMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNT--CEEYHTVGHPSCHIPKD-LAL 206
DB 35 DKETFTCWNPNGSDGG--LPTNYSLYTSKE--GEKNTYECPDYKTSKSPNCSFFSKQYTSI 90

QY 207 FPTYEIWEATNRLGARSDDLTLVDLVVTTDPPDPDVHVSRLVGLPPEKPFNISCWSR 264
DB 91 WKIYIITVNATNMGSSSDPLYVDVTVIVBPEPPNLT-L-EVKQLKDKKTYLWYKWLPP 149

RESULT 14
I53269
prolactin receptor, long form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I53269; J0671; S34356
R;Clarke, D.L.; Linzer, D.I.H.
Endocrinology 133, 224-232, 1993
A;Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
A;Reference number: I53269; MUID:93307149; PMID:8319571
A;Accession: I53269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-608 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020E90; GB:L14811; NID:g293769; PIDN:
R;Moore, R.C.; Oka, T.
Gene 134, 263-265, 1993
A;Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
A;Reference number: J0671; MUID:94085788; PMID:8262385
A;Accession: J0671
A;Molecule type: mRNA
A;Residues: 1-608 <MOO>
A;Cross-references: UNIPARC:UPI0000020E90; GB:L13593; NID:g347398; PIDN:AAC37641.1; PID
R;Edery, M.; Peret, A.; Nandi, S.; Kelly, P.A.
submitted to the EMBL Data Library, June 1993
A;Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
A;Reference number: S34356

C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36116
R;Shioto, M.; Banville, D.; Ali, S.; Jolicœur, C.; Boutin, J.M.; Ederly, M.; Djiane, J.
Mol. Endocrinol. 4, 1136-1143, 1990
A;Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A;Reference number: A36116; MUID:91155946; PMID:2293022
A;Accession: A36116
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-610 <SHI>
A;Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170ADB; GB:M57668; NID:g206366; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 312; DB 2; Length 610;
Best Local Similarity 35.4%; Pred. No. 2.1e-16;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

QY 125 SILAGSLYGLPPEKPFNISCWSRNKMLTCTWTPGAHGETFLHTNYSKYKLRWYQD 184
DB 15 SLKQGS-----PPGKPEIHKCRSPDKETFTCWNPFGTDGG--LPTNYSLYTSKE--GEK 65

QY 185 NT--CEEYHTVGHPSCHIPKD-LALPTPEIWEATNRLGARSDDLTLVDLVVTTDPP 241
DB 66 TTYECPDYKTSKSPNCSFFSKQYTSIWKIYIITVNATNMGSSSDPLYVDVTVIVBPEPP 125

QY 242 PDVHVSRLVGLPPEKPFNISCWSRNKMLTCTWTPGAHGETFLHTNYSKYKLRWYQD 296
DB 126 RNLTL-EVKQLKDKKTYLWYKWSPTITDVKTCWFTWEYIRLKPBAEWE-IHFTGHQ 183

QY 297 TSCRLAGLPGTVYFVQVRCNPPFGIYGSKKAGIWSWSHPTAATP 342
DB 184 TQPKVFDLYPGQKYLQVTRCKP-----DHGYWSRWSQESSVEMP 222

RESULT 12
I77525
prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I77525
R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the prolactin receptor in mouse liver.
A;Reference number: I57699; MUID:89261824; PMID:2725531
A;Accession: I77525
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-292 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B198; GB:M22959; NID:g200481; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 307.5; DB 2; Length 292;
Best Local Similarity 32.8%; Pred. No. 1.8e-16;
Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

QY 90 LSRLMTSTLALANLNGSRQSGDNLVCHARDGSIAGSLYGLPPEKPFNISCWSR 149
DB 1 MSSALAYMLLVLSISLNG--QS-----PPGKPEIHKCRSP 34

QY 150 NMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNT--CEEYHTVGHPSCHIPKD-LAL 206
DB 35 DKETFTCWNPNGSDGG--LPTNYSLYTSKE--GEKNTYECPDYKTSKSPNCSFFSKQYTSI 90

QY 207 FPTYEIWEATNRLGARSDDLTLVDLVVTTDPPDPDVHVSRLVGLPPEKPFNISCWSR 264
DB 91 WKIYIITVNATNMGSSSDPLYVDVTVIVBPEPPNLT-L-EVKQLKDKKTYLWYKWLPP 149

QY 265 ALKDF---LFQAKYQIRYRVEDSDWKVDDVSNQTSCLAGLKPGTVYFVQVRCNPF 321
DB 150 TITDVKTCWFTWEYIRLKSSEADEWE-IHFTGHQTFQKVFDFLYPGQKYLQVTRCKP--- 205

QY 322 YGSKKAGIWSWSHPTAATP 342

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: April 11, 2006, 02:04:23 ; Search time 123.014 Seconds
(without alignments)
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Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1422.5	63.2	389	2 Q6DG28_BRARE	Q6dg28 brachydanio
4	1382.5	61.4	394	2 Q6UQ05_TETNG	Q6uq05 tetraodon n
5	995	44.2	437	2 Q4RMP5_TETNG	Q4rmp5 tetraodon n
6	468.5	20.8	207	2 Q4TCM7_TETNG	Q4tcm7 tetraodon n
7	416	18.5	151	2 Q4RDR1_TETNG	Q4rdr1 tetraodon n
8	380	16.9	199	2 Q4RDQ9_TETNG	Q4rdq9 tetraodon n
9	371	16.5	918	2 Q9W6U9_CHICK	Q9w6u9 gallus gall
10	355.5	15.8	881	2 O57519_XENLA	O57519 xenopus lae
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12	331	14.7	288	2 Q96P36_HUMAN	Q96p36 homo sapien
13	331	14.7	349	2 Q9UHJ5_HUMAN	Q9uhj5 homo sapien
14	331	14.7	376	2 Q96P35_HUMAN	Q96p35 homo sapien
15	331	14.7	622	1 PR1R_HUMAN	P16471 homo sapien
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17	330.5	14.7	1010	2 Q77Q89_RAT	Q7tq89 rattus norv
18	329	14.6	857	2 Q5FC04_HUMAN	Q5fc04 homo sapien
19	329	14.6	918	1 ILGRB_HUMAN	P40189 homo sapien
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21	319.5	14.2	917	2 Q6PD15_MOUSE	Q6pd19 mus musculus
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23	316	14.0	622	2 Q9N0J7_CALJA	Q9n0j7 callithrix
24	314.5	14.0	608	2 Q99JZ1_MOUSE	Q99jz1 mus musculus
25	314	13.9	622	2 Q865V4_CEBAP	Q865v4 cebus apell
26	314	13.9	830	1 PR1R_COLLI	Q90374 columba liv
27	312	13.9	310	2 Q5BDZ7_RAT	Q5bdz7 rattus norv
28	312	13.9	610	1 PR1R_RAT	P05710 rattus norv
29	307.5	13.7	292	2 Q8C7G1_MOUSE	Q8c7g1 mus musculus
30	307.5	13.7	608	1 PR1R_MOUSE	Q08501 mus musculus
31	307.5	13.7	616	1 PR1R_RABIT	P14787 oryctolagus

32	307	13.6	625	1 PR1R_PIG	Q6jta8 sus scrofa
33	306	13.6	460	2 Q7T2Z0_CHICK	Q7t2z0 gallus gall
34	306	13.6	581	1 PR1R_SHEEP	O46561 ovis aries
35	306	13.6	831	1 PR1R_CHICK	O04594 gallus gall
36	306	13.6	831	2 Q6QDA0_CHICK	Q6qda0 gallus gall
37	305	13.5	831	1 PR1R_MELGA	Q91094 meleagris g
38	303	13.5	581	1 PR1R_CEREL	Q28235 cervus elap
39	302.5	13.4	581	1 PR1R_BOVIN	Q28172 bos taurus
40	294	13.1	611	2 Q9PTH9_XENLA	Q9pth9 xenopus lae
41	289.5	12.9	604	2 Q6UAP8_TETNG	Q6uap8 tetraodon n
42	289	12.8	357	2 Q4SQD8_TETNG	Q4sqd8 tetraodon n
43	289	12.8	819	2 Q616F7_XENLA	Q616f7 eublepharis
44	288.5	12.8	611	2 Q91BF6_XENLA	Q91bf6 xenopus lae
45	288.5	12.8	611	2 Q9PTI0_XENLA	Q9pti0 xenopus lae

ALIGNMENTS

RESULT 1
CRLF1_MOUSE
ID CRLF1_MOUSE STANDARD; PRT; 425 AA.
AC Q9Jm58;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)
DE (CLF-1) (Cytokine receptor-like molecule 3) (CRLM-3) (NR6).
GN Name=Crlf1; Synonyms=Crlm3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hiroyana T., Iwana A., Nakamura Y., Nakauchi H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RX FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed10359701; DOI=10.1016/S0960-9822(99)80266-8;
RA Alexander W.S., Raker S., Robb L., Farley A., Willson T.A.,
Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,
Hasegawa M., Maeda M., Fabri L., Jachno K., Nash A., Metcalf D.,
Nicola N.A., Hilton D.J.;
RT "Suckling defect in mice lacking the soluble haemopoietin receptor NR6.";
RL Curr. Biol. 9:605-608 (1999).
RN [3]
RP PHOSPHORYLATION SITE SER-222.
RX PubMed15378723; DOI=10.1002/tcm.1604;
RA Jin W.-H., Dai J., Zhou H., Xia Q.-C., Zou H.-P., Zeng R.;
RT "Phosphoproteome analysis of mouse liver using immobilized metal affinity purification and linear ion trap mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 18:2169-2176 (2004).
CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory role in the immune system and during fetal development. May be involved in nervous system development (By similarity). Plays an essential role in the initiation and/or maintenance of suckling in neonatal mice.
CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a heteromeric complex with cardiotrophin-like cytokine (CLC); the CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor receptor (CNTFR) (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected in the brain of adult mice.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein folding and thereby efficient intracellular transport and cell-surface receptor binding.
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3 subfamily.
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL: AB040038; BAA92777.1; -, mRNA.

DR HSP; P40223; ICD9.

DR Ensembl; ENSMUSG0000007888; Mus musculus.

DR MGI; MGI:1340030; Crfl1.

DR GO; GO:0005615; C:extracellular space; TAS.

DR InterPro; IPR002996; Cytok recept_B/G.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00041; fn3; 2.

DR SMART; SM00060; FN3; 2.

DR PROSITE; PS50853; FN3; 2.

DR PROSITE; PS50835; IG LIKE; FALSE NEG.

KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;

KW Repeat; Signal.

FT SIGNAL 1 33 Potential.

FT CHAIN 34 425 Cytokine receptor-like factor 1.

FT DOMAIN 35 134 Ig-like C2-type.

FT DOMAIN 137 232 Fibronectin type-III 1.

FT DOMAIN 237 337 Fibronectin type-III 2.

FT MOTIF 330 334 WXSWS motif.

FT MOD_RES 222 222 Phosphoserine.

FT CARBOHYD 95 95 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 107 107 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 143 143 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 171 171 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 295 295 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 385 385 N-linked (GlcNAc. .) (Potential).

FT DISULFID 146 156 By similarity.

FT DISULFID 187 198 By similarity.

FT SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 98.9%; Score 2226.5; DB 1; Length 425;
Best Local Similarity 98.8%; Pred. No. 1.8e-168;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRGPVQAQARRPRPLSSLSWSPLLCLVGPVGGSGAHTAVISPDPTLLIGSSLQ 60
|||||
DB 1 MPAGRGPVQAQARRPRPLSSLSWSPLLCLVGPVGGSGAHTAVISPDPTLLIGSSLQ 60
|||||

QY 61 ATCSIHGDTPGAEGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
|||||
DB 61 ATCSIHGDTPGAEGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
|||||

QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNMKDLTCRWTPGAGETFLHTNYSCLKLRW 180
|||||
DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNMKDLTCRWTPGAGETFLHTNYSCLKLRW 180
|||||

QY 181 YGQDNTECEVHTVGRHSCHIPKDALFTPEIWEATNRLGARSVDLTLDLVDDVTDP 240
|||||
DB 181 YGQDNTECEVHTVGRHSCHIPKDALFTPEIWEATNRLGARSVDLTLDLVDDVTDP 240
|||||

QY 241 PPDVHVSRVGGLDQLSVRWVSPALPKDFLQAKYQIYRYVEDSDVKVVDVDSNQTSCR 300
|||||
DB 241 PPDVHVSRVGGLDQLSVRWVSPALPKDFLQAKYQIYRYVEDSDVKVVDVDSNQTSCR 300
|||||

QY 301 LAGLKPCTVTVQVRCNPFYIGSKAGIWSWSHTAATPSRSPGPGGVCERPGGE 360
|||||
DB 301 LAGLKPCTVTVQVRCNPFYIGSKAGIWSWSHTAATPSRSPGPGGVCERPGGE 360
|||||

QY 361 PSSGPVRELEKQFLGWLKKHAYCSNLSFRLYDQRAWQKSHKTRNQ---VLPA 411
||||| : : :
DB 361 PSSGPVRELEKQFLGWLKKHAYCSNLSFRLYDQRAWQKSHKTRNQDEGILPS 414
|||||

RESULT 2
CRLF1 HUMAN STANDARD; PRT; 422 AA.
ID CRLF1_HUMAN
AC O75462; Q9UHH5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)
DE (CFLF-1) (Zcytor5).
GN Name=CRLF1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY AND INDUCTION.
RC TISSUE=Fetal lung;
RX MEDLINE=98349389; PubMed=9686600;
RA Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;
RT "Cytokine-like factor-1, a novel soluble protein, shares homology with
RT members of the cytokine type I receptor family.";
RT J. Immunol. 161:1371-1379(1998).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hemopoietic cytokine receptor domains";
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL [3]
RN NUCLEOTIDE SEQUENCE.
RA Lok S., Presnell S.R., Jellmberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RL [4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uslan T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heintz E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PROTEIN SEQUENCE OF 38-52
 RX PubMed=15340161; DOI=10.1101/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RA "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites";
 RL Protein Sci. 13:2819-2824(2004).
 RN [7]
 RP INTERACTIONS WITH CLC AND CNTRP.
 RX MEDLINE=20423191; PubMed=1096616; DOI=10.1038/78765;
 RA Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau H.,
 RA Froger J., Suard I., de Coignac A.B., Delneste Y., Bonnefoy J.Y.,
 RA Gauchat J.-F., Gascan H.;
 RT "CLF associates with CLC to form a functional heteromeric ligand for
 RT the CNTP receptor complex.";
 RL Nat. Neurosci. 3:867-872(2000).
 RN [8]
 RP VARIANTS CISS HIS-81 AND ARG-374.
 RX MEDLINE=22428294; PubMed=12509788;
 RA Knappskog P.M., Majewski J., Livneh A., Nilsson P.T.E., Bringsli J.S.,
 RA Ott J., Boman H.;
 RT "Cold-induced sweating syndrome is caused by mutations in the CRLF1
 RT gene.";
 RL Am. J. Hum. Genet. 72:375-383(2003).
 CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory
 CC role in the immune system and during fetal development. May be
 CC involved in nervous system development.
 CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a
 CC heteromeric complex with cardiotrophin-like cytokine (CLC); the
 CC CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor
 CC receptor (CNTRP).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highest levels of expression observed in
 CC spleen, thymus, lymph node, appendix, bone marrow, stomach,
 CC placenta, heart, thyroid and ovary. Strongly expressed also in
 CC fetal lung.
 CC -!- INDUCTION: Up-regulated in fibroblast primary cell cultures under
 CC stimulation by IFN-gamma, TNF-alpha and IL-6.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -!- DISEASE: Defects in CRLF1 are the cause of cold-induced sweating
 CC syndrome (CISS) [MIM:272430]. CISS is an autosomal recessive
 CC disorder characterized by profuse sweating induced by cool
 CC surroundings (temperatures of 7 to 18 degrees Celsius). Additional
 CC abnormalities include a high-arched palate, nasal voice, depressed
 CC nasal bridge, inability to fully extend the elbows and
 CC kyphoscoliosis.
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
 CC subfamily.
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 CC domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF059293; AAC38335.1; -; mRNA.
 CC EMBL; AF073515; AAD39681.1; -; mRNA.
 CC EMBL; AF178684; AAD54385.1; -; mRNA.
 CC EMBL; AY358291; AAQ88658.1; -; mRNA.
 CC EMBL; BC044634; AAH44634.1; -; mRNA.
 CC HSP; P40223; 1CD9.
 CC Ensembl; ENSG0000006016; Homo sapiens.
 CC HGNC; HGNC:2364; CRLF1.
 CC MIM; 604237; -.
 CC MIM; 272430; -.

DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0019955; F:cytokine binding; IPI.
 DR GO; GO:0004872; P:receptor activity; TAS.
 DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . . ; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00041; fn3; 2.
 DR PROSITE; PS0853; FN3; 2.
 DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
 KW Direct protein sequencing; Disease mutation; Glycoprotein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.
 FT SIGNAL 1 37
 FT CHAIN 38 422 Cytokine receptor-like factor 1.
 FT DOMAIN 38 131 Ig-like C2-type.
 FT DOMAIN 134 229 Fibronectin type-III 1.
 FT DOMAIN 234 334 Fibronectin type-III 2.
 FT MOTIF 327 331 WSXWS motif.
 FT MOD_RES 219 219 Phosphoserine (By similarity).
 FT CARBOHYD 92 92 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 104 104 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 140 140 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 168 168 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 292 292 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 382 382 N-linked (GlcNAc . .) (Potential).
 FT DISULFID 143 153 By similarity.
 FT DISULFID 184 195 By similarity.
 FT VARIANT 81 81 R -> H (in CISS).
 FT VARIANT 374 374 /FTID=VAR_017865.
 FT VARIANT 240 240 L -> R (in CISS).
 FT CONFLICT 240 240 D -> E (in Ref. 3).
 SQ SEQUENCE 422 AA; 46302 MW; AD9DFECB01B84228 CRC64;

Query Match 93.1%; Score 2096; DB 1; Length 422;
 Best Local Similarity 93.7%; Pred. No. 4.3e-158;

Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPGVAGSARPPRLSLPLLLCVLGVPRGGSGAHTAVISPODPTLLIGSSIQ 60
 DB 1 MPAGRGPAGSARPP-PLLP-LL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57
 QY 61 ATCSIHGTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 58 ATCSVHGPPGATAGLYWTNGRLPPELSRLVNLALANLNGSRQSGDNLVCH 117
 QY 121 ARDGSILAGSLYGLPPEKPFNISCWRNMKDLTCRWTPGAHGTFLHTNYSKYKLRW 180
 DB 118 ARDGSILAGSLYGLPPEKPFNISCWRNMKDLTCRWTPGAHGTFLHTNYSKYKLRW 177
 QY 181 YGQDNTCEYHTVGPHSCHIPKDLALFPYELWVETNRLGSARSDVLTLDVLDVVTDP 240
 DB 178 YGQDNTCEYHTVGPHSCHIPKDLALFPYELWVETNRLGSARSDVLTLDVLDVVTDP 237
 QY 241 PPDVHVSRVGGLDQLSVRWVSPALKDFLQAKYQIRYRVEDSVDMKVVDDVSNQTSR 300
 DB 238 PPDVHVSRVGGLDQLSVRWVSPALKDFLQAKYQIRYRVEDSVDMKVVDDVSNQTSR 297
 QY 301 LAGLPGTVYVQVRCNPFYIGSKAGIWSHPTAATSRSRPFGGVCPRGGE 360
 DB 298 LAGLPGTVYVQVRCNPFYIGSKAGIWSHPTAATSRSRPFGGVCPRGGE 357
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSPLRYDQWRAMWOKSHKTNQ---VLPA 411
 DB 358 PSSGPVRELKQFLGWLKKHAYCSNLSPLRYDQWRAMWOKSHKTRNDEGILPS 411

RESULT 3

Q6DG28 BRARE
 ID Q6DG28 BRARE PRELIMINARY; PRT; 389 AA.
 AC Q6DG28;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT	25-OCT-2004 (TReMBLrel. 28, Last annotation update)	
DE	Zgc:91992.	
GN	ORFNames=zgc:91992;	
OS	Brachydanio rerio (zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI TaxID=7955;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Whole;	
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Whole;	
RA	Strausberg R.	
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.	
CC	-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein	
CC	folding and thereby efficient intracellular transport and cell-	
CC	surface receptor binding (By similarity).	
DR	EMBL; BC076526; AAH76526.1; -; mRNA.	
DR	ZFIN; ZDB-GENE-040718-397; Zgc:91992.	
DR	InterPro; IPR002996; Cytnk_recept_B/G.	
DR	InterPro; IPR003961; FN_III.	
DR	Pfam; PF00041; fn3; 1.	
DR	SMART; SM00060; FN3; 2.	
DR	PROSITE; PS50853; FN3; 2.	
KW	Receptor; Repeat; Transmembrane.	
SEQ	SEQUENCE 389 AA; 43314 MW; E30903B99639864A CRC64;	
	Query Match 63.2%; Score 1422.5; DB 2; Length 389;	
	Best Local Similarity 68.2%; Pred. No. 1.4e-104;	
	Matches 262; Conservative 48; Mismatches 67; Indels 7; Gaps 5;	
QY	27 LLLCVLGVPRGSGAHTAVISQDPTLLIGSSLOATCSIHGTPPGATAGLYWTNGRRLL 86	
Db	7 LHLCAAGVL--SSSTQVATVPQDPALLIGSSLTATCSVNPDP-HGIHAGSLWTNGKRL 63	
QY	87 PSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLTAGSCLYVGLPPEKPNISC 146	
Db	64 PSSTYSLSPVTSVTLPRLSGSRQSGDNLVCHNGGHVLAGSCIVGMPPKPNLTC 123	
QY	147 WSNMMDLTCRWTPGAHGETFLHTNTSLKYLKWYGDNTCEBYHTVGPCHSKIPKDAL 206	
Db	124 WSNMMDLTCRWAPGGGGETFIKTKYLKWLWYGEKECEDYSTGEPTCYIPRDAL 183	
QY	207 FTFYELWEATNRLGARSVDLFDLVDTVTTPDPDVHVSVRVGGLEDQLSVRWVSPPAL 266	
Db	184 FTFYELWEASNLGTATSDVILDLVDTVTTPDPDVHVSVRVGGLEDQLTVRWGTPPAL 243	
QY	267 KDFLFQAKYQIRVRVEDSVKVVDDVSNQTSCLAGLKPGTVYFVQVRCNPGIYGSKK 326	
Db	244 KDFLFQAKYQIRYRLDESSDWKVVDDVGNQTSCLAGLRFGTVFVQVRCNPGIYGSRK 303	

QY	327 AGIWESEHPTAASTPRSERPGGVCYCEPSSGPPVRELKQFLGWLKKHAY--CSN 385	
Db	304 AGIWESEHPTAASTPRSERPGGVCYCEPSSGPPVRELKQFLGWLKKHAYGCSG 360	
QY	386 LSFRLYDQWRAMWOKSHKTRNQVL 409	
Db	361 MSIKLYDQWRVWLQSHKTRNQVL 384	

RESULT 4

Q6UA05	TETNG	
ID	Q6UA05_TETNG PRELIMINARY;	PRT; 394 AA.
AC	Q6UA05;	
DT	05-JUL-2004 (TReMBLrel. 27, Created)	
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)	
DE	Class I helical cytokine receptor number 1.	
GN	Name=CRPAI;	
OS	Tetraodon nigroviridis (Green puffer).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	
OC	Acanthopterygia; Acanthopterygii; Percomorpha; Tetraodontiformes;	
OC	Tetraodontidae; Tetraodontidae; Tetraodon.	
OX	NCBI_TaxID=99883;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RX	PubMed=15496914; DOI=10.1038/nature03025;	
RA	Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,	
RA	Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,	
RA	Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,	
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,	
RA	Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,	
RA	Bilmonet C., Skalli Z., Cattolico L., Poulain J., Berardinis Vd.,	
RA	Cruaud C., Duprat S., Bottier P., Coutanceau J.-P., Gouzy J.,	
RA	Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,	
RA	Kellis M., Wolff J.-N., Guigs R., Zody M.C., Mesirov J.,	
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,	
RA	Laudet V., Schachter V., Quittier F., Saurin W., Scarpelli C.,	
RA	Wincker P., Lander E.S., Weissenbach J., Crolious H.R.;	
RT	"Genome duplication in the teleost fish Tetraodon nigroviridis reveals	
RT	the early vertebrate proto-karyotype."	
RL	Nature 431:946-957 (2004).	
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By	
CC	similarity).	
CC	-!- DOMAIN: The WSXWS motif appears to be necessary for proper protein	
CC	folding and thereby efficient intracellular transport and cell-	
CC	surface receptor binding (By similarity).	
DR	EMBL; AY374473; AAR25664.1; -; mRNA.	
DR	Ensembl; AY374473; Tetraodon nigroviridis.	
DR	GO; GO:004872; F:receptor activity; IEA.	
DR	InterPro; IPR002996; Cytnk_recept_B/G.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR007110; Ig-like.	
DR	Pfam; PF00041; fn3; 2.	
DR	SMART; SM00060; FN3; 2.	
DR	PROSITE; PS50853; FN3; 2.	
DR	PROSITE; PS50835; IG_LIKE; 1.	
KW	Immunoglobulin domain; Receptor; Repeat; Transmembrane.	
SEQ	SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;	
	Query Match 61.4%; Score 1382.5; DB 2; Length 394;	
	Best Local Similarity 67.7%; Pred. No. 2.2e-101;	
	Matches 260; Conservative 39; Mismatches 80; Indels 5; Gaps 4;	
QY	27 LLLCVLGVPRG--GSGAHTAVISQDPTLLIGSSLOATCSIHGTPPGATAGLYWTNGRR 85	
Db	9 LLLLIHSPAVLALSTHVAIVYQDFVLRGNSNLTASCIWRSDL-GVHASSLFWTLNGQP 67	
QY	86 LPSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLTAGSCLYVGLPPEKPNIS 145	
Db	68 LPSSLYRVLSPTNLVTLAGLNASRQTSQDNLVCHHHKHILAGSLCYVGMPPKPNLT 127	

QY 146 CWSRNKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPHSCHIPKDLA 205
 DB 128 CWSRNKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPHSCHIPKDLA 187
 QY 206 LFTPEIWEATNRLGASRSDVLTDLVDVTTDPDPVHVSRVGGLEDQLSVRVWSPPA 265
 DB 188 LFTPEIWEATNRLGASRSDVLTDLVDVTTDPDPVHVSRVGGLEDQLSVRVWSPPA 247
 QY 266 LKDFLFOAKYQIRYRVEDSDVWVDDVSNQTSCLAGLKPCTVYVQVRCNPPFGYGSK 325
 DB 248 LKDFLFOAKYQIRYRVEDSDVWVDDVSNQTSCLAGLKPCTVYVQVRCNPPFGYGSK 307
 QY 326 KAGINSEWHPHTAASRPRPGCGVCEPRGSGPVRRELKQFLGWLKXHY-CS 384
 DB 308 KAGINSEWHPHTAASRPRPGCGVCEPRGSGPVRRELKQFLGWLKXHY-CS 365
 QY 385 NLSFRLYDQWRAWMOXSHKTRNOV 408
 DB 366 SMSMKLYDQWRLVMQXSHKARNOV 389

RESULT 5

Q4RMP5_TETNG
 ID Q4RMP5_TETNG PRELIMINARY; PRT; 437 AA.
 AC Q4RMP5;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Chromosome 10 SCAR15019, whole genome shotgun sequence.
 DE (Fragment).
 DE ORFNames=GSTENG00031935001;
 GN Tetraodon nigroviridis (Green puffer).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; CAAE01015019; CAG10337.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 437 AA; 49065 MW; 99F9602E88F95583 CRC64;

Query Match 44.2%; Score 995; DB 2; Length 437;
 Best Local Similarity 53.8%; Pred. No. 1.6e-70;
 Matches 199; Conservative 33; Mismatches 62; Indels 76; Gaps 5;
 QY 44 AVTSPDPTLLTGSSLOATCSHGDTPTGATAGLWTLNGRLPSELSTLSTLALAL 103
 DB 1 AVTSPDPTLLTGSSLOATCSHGDTPTGATAGLWTLNGRLPSELSTLSTLALAL 59

QY 104 ANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAH 163
 DB 60 AGLNASROTSGDNLVCHHKGHILAGSCLYVGMPPAKPVNLTCSWSTKDLTCSWAPGGR 119
 QY 164 GTEFLHTNYSKYKLRWYQDNTCEYHTVGPHSCHIPKDLAFTPEIWEATNRLGSA 223
 DB 120 GTHISTQYTLKLRWYQDNTCEYHTVGPHSCHIPKDLAFTPEIWEATNRLGSA 179
 QY 224 RSDVLTDLVDVTTDPDPVHVSRVGGLEDQLSVRVWSPPAKDLFOAKYQIRYRVED 283
 DB 180 TSDVITLTDLDVTTDPDPVHVSRVGGLEDQLSVRVWSPPAKDLFOAKYQIRYRVED 239
 QY 284 SDVWK-----VWDD 292
 DB 240 SDQWKEKSAFQDERERAWTEPLCILGLVLMNEKYSVEAGPLQMALRLILLPVLWVMD 299
 QY 293 VSNQTSCLAGLKPCTVYVQVRCNPPFGYGSKAG-----INSEWHPHTAASRPRPG 348
 DB 300 VGNQTSCLAGLKPCTVYVQV-----GPRSSASDRITW-----SDRRV 339
 QY 349 PGGGVCEPRG 358
 DB 340 ASAGPLQPRG 349

RESULT 6

Q4TCM7_TETNG
 ID Q4TCM7_TETNG PRELIMINARY; PRT; 207 AA.
 AC Q4TCM7_TETNG
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAP6801, whole genome shotgun sequence.
 DE (Fragment).
 DE ORFNames=GSTENG00003230001;
 GN Tetraodon nigroviridis (Green puffer).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; CAAE01006801; CAF89355.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 207 AA; 22607 MW; 71F8E80B9998309F CRC64;

Query Match 20.8%; Score 468.5; DB 2; Length 207;
 Best Local Similarity 48.3%; Pred. No. 4.6e-29;
 Matches 102; Conservative 7; Mismatches 21; Indels 81; Gaps 4;

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QY 231 DVLDDVTTDPDPVHVSVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVDSVDWK-- 288
DB 1 ECLPPVTTDPSPGVTYSRVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVDSVDWKEE 60
QY 289 -----VDDVSNQTS 299
DB 61 KSAFQERERAWTEPLCILGLRLVLMNEKYVSAGPLQWALLRILLPVLWMDVGNQTS 120
QY 300 RLGLKPGTVY-----FVQVRCNPFYIGSKKAGIWSHPT 337
DB 121 RLGLRPGTVYSRWDPGPAPQTGSGSLTAVSLPQVRCNPFYIGSKKAGIWSHPT 180
QY 338 AASTPRSERP-----GPGGVGVCBPGGEPSSG 364
DB 181 AASTPHSGEPPLPAGPGRSL-----GSAPPSG 207

RESULT 7
Q4RD1 TETNG PRELIMINARY; PRT; 151 AA.
AC Q4RD1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15947, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00037335001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01015947; CAG13471.1; -; Genomic_DNA.
DR NON_TER 151
FT SEQUENCE 151 AA; 16177 MW; 14AD74333A6C7F90 CRC64;
SQ
Query Match 18.5%; Score 416; DB 2; Length 151;
Best Local Similarity 58.0%; Pred. No. 4.6e-25;
Matches 80; Conservative 15; Mismatches 37; Indels 6; Gaps 2;

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QY 29 LCVLGVPRGGSGAHTAVISQDPTLLIGSSLIQATCSIHGDTPTCATAGLWTWTLNGLRPLS 88
DB 20 VCVV-----GHPDPVAVESQDPVLPFTGSSLTATCTLSPEL-RLLSALYWTWTLNGLTFLS 73
QY 89 ELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSLYGLPPEKPFNTSCWS 148
DB 74 STYGRLLGPHTLSTLWHLNLSRQSGDNLVCHSDGHVLACGLYGMPPKPNLTCWS 133

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QY 149 RNKDLTCRWTPGAGHET 166
DB 134 RNTKDLSCRWRPFGILGET 151

RESULT 8
Q4RD9 TETNG PRELIMINARY; PRT; 199 AA.
AC Q4RD9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15948, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00037750001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01015948; CAG13473.1; -; Genomic_DNA.
DR NON_TER 1
FT SEQUENCE 199 AA; 21734 MW; 299786CDFB24BDEB CRC64;
SQ
Query Match 16.9%; Score 380; DB 2; Length 199;
Best Local Similarity 67.0%; Pred. No. 4.7e-22;
Matches 73; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

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QY 236 VTTDPPDVHVSVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVDSVDWKVDDVSN 295
DB 34 VTTDPTDVHVSVRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVDSVDWKVDDVSN 87
QY 296 QTSCLAGLKPQTVYFVQVRCNPFYIGSKKAGIWSHPTAAPTSPS 344
DB 88 -----SVLWTVHFVQVRCNPFYIGSKKAGIWSHPTAAPTSPS 128

RESULT 9
Q9W6U9 CHICK PRELIMINARY; PRT; 918 AA.
AC Q9W6U9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glycoprotein 130 precursor.
GN Name=Gp130;
OS Gallus gallus (Chicken).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryonic heart primary culture;
 RX MEDLINE=99026068; PubMed=9806927;
 RA Geissen M., Heller S., Pennica D., Ernberger U., Rohrer H.;
 RT "The specification of sympathetic neurotransmitter phenotype depends
 on gp130 cytokine receptor signaling.";
 RL Development 125:4791-4801(1998).
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 folding and thereby efficient intracellular transport and cell-
 surface receptor binding (By similarity).
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 activation (By similarity).
 CC EMBL: AJ011688; CAB42084.1; -; mRNA.
 DR HSP; P40189; IBQ9.
 DR InterPro: IPR002996; Cytn_recept_B/G.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtrecept_1302.
 DR InterPro: IPR010457; Lep_receptor_Ig.
 DR Pfam: PF00041; fn3; 4.
 DR SMART; SM00060; FN3; 4.
 DR PROSITE; PS00853; FN3; 5.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 SQ SEQUENCE 918 AA; 102495 MW; FE7625FF3E3613EF CRC64;
 Query Match 16.5%; Score 371; DB 2; Length 918;
 Best Local Similarity 30.2%; Pred. No. 1.7e-20;
 Matches 111; Conservative 41; Mismatches 138; Indels 78; Gaps 16;
 QY 27 LLLCVLGVPRGSGAHTAVISQDPTLLIGSLQATCSIHG---DTPGATAGLYWTLNG 83
 Db 16 LNICSEFV-SGGVLQSCGHIIPESPVALGSGNFTALCILNESCLDRGNIAQIWMKN 74
 QY 84 RLPSLSLLN-----TSTLALALANLNGSRQSGDNLVCHA-RDGSI---LAG 129
 Db 75 KVIPKEQYREINRTVSSVTFNDTSLA-----SPLTCNVLADGQIEQNIYG 120
 QY 130 SCLVGLPPEKPFNTSC-----WSRNMKDLTCRWTPGAHGETFLHTNYSKYKLW 180
 Db 121 ISVTGLPPEKPNLSVILSPKVEWYN-----CTWNPGRH--TFDTRFLKTMWPR 173
 QY 181 YGQDNTCEYHTVGPCHSKIPKDLALFTPYEIVWEATNRLGARSQDVLTLVDVVVTTDP 240
 Db 174 ETFFDCIPEYVN---NSCTI-SDVQPFVNLEWVEAANALGKAESDHLVDFDIEIVKPP 229
 QY 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYRVEDSDWKV---DVSNQ 297
 Db 230 PRLSVNS-GILPTVLKLSWEN-QISTVVMELKNIRYRISGDTNMEVPPEDTASPT 286
 QY 298 SCLAGLKPGTYFVQVRCNPGIYGSKKAGIWESEHPTASTPRSRPFGGGVCEPR 357
 Db 287 SFSIQGLRPYTYFVSIRC-----MKEDGVGFWSMDSEEQIGVTTED----- 328
 QY 358 GGPSPSGP 365
 Db 329 --KPSKGP 334
 RESULT 10
 O57519 XENLA
 ID O57519_XENLA PRELIMINARY; PRT; 881 AA.
 AC O57519
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Gp130p1.

GN Name=xgpl30;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Chen J., Grace A., Chien K.R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 folding and thereby efficient intracellular transport and cell-
 surface receptor binding (By similarity).
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 activation (By similarity).
 CC EMBL: AF041845; AAC03531.1; -; mRNA.
 DR HSP; P40189; IBQ9.
 DR InterPro: IPR002996; Cytn_recept_B/G.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtrecept_1302.
 DR InterPro: IPR010457; Lep_receptor_Ig.
 DR Pfam: PF00041; fn3; 4.
 DR SMART; SM00060; FN3; 4.
 DR PROSITE; PS00853; FN3; 5.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 KW Receptor; Repeat; Transmembrane.
 SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;
 Query Match 15.8%; Score 355.5; DB 2; Length 881;
 Best Local Similarity 30.5%; Pred. No. 2.8e-19;
 Matches 100; Conservative 43; Mismatches 136; Indels 49; Gaps 11;
 QY 50 DPTLLIGS-SLOATCSIHGDTPGATAGLYWTLNGRLPSLSRLNTSTLALANLNG 108
 Db 33 DPGIVHGERPFTAYCINQTCLEBDAKRIYKLVKGVKPEYQYELNQTSSVTFENLT 92
 QY 109 SRQSGDNLVCHARDGSLAGSLVGLPPEKPFNTSCWRNMKDLTCRWTPGAHGETFL 168
 Db 93 LNSPLTCNVMSAGHVANTLYGIFFLGLPDPKFTNLTCIYVQDNLCTCTWDFGR--PTNL 150
 QY 169 HTNYSKYKLW-----YGQDNTCEYHTVGPCHSKIPKDLALFTPYEIVWEATNRL 220
 Db 151 PTNYTLSH--RWAHFGANYCRGANNSC-----TIHSP-GFQFYIDTTFOVEATNEL 198
 QY 221 GSARSDVLTLDVLDVVVTTDPDPPDVHVSVRVGGLEDQLSVRWVSPALKDPLFOAKYQIRYR 280
 Db 199 GIQKSETLTIDPVNIVKPNPQLSELISLELPNALKIEWKNPIT---NAFNLKYNIRYR 255
 QY 281 VEDSDWKV---DVSNQTSCLAGLKPGTYFVQVRCNPGIYGSKKAGIWESEHPT 337
 Db 256 PVKQDWEVPEEDTASHRDSFTLQDLLPNTVYVSIRC-----THKDHGFWSMDSELK 310
 QY 338 AASTPRSRPFGGGVCEPRGSPSGP 365
 Db 311 KQVTP--EAP-----PSRGP 323
 RESULT 11
 Q8TD78 HUMAN
 ID Q8TD78_HUMAN PRELIMINARY; PRT; 268 AA.
 AC Q8TD78
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Prolactin receptor delta 7/11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=breast tumor;
RA Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC EMBL; AF492470; AML18048.1; -; mRNA.
DR HSSP; P16471; 1BP3.
DR SMR; Q87D78; 29-227.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; HemptreceptL_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS0853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 268 AA; 30705 MW; FBB498AB649A078C CRC64;
Query Match 14.7%; Score 332; DB 2; Length 268;
Best Local Similarity 37.0%; Pred. No. 4.5e-18;
Matches 84; Conservative 28; Mismatches 97; Indels 18; Gaps 8;
QY 126 ILAGSCLYVG-LPPEKPFNISCWSNMKDLTCRWTPGAHGETFLHNTYSLKYKLRWYGD 184
DB 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTYHREGETLM 72
QY 185 NTCEEYHTVGHPSCHIPKD-LALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDPPPD 243
DB 73 HCEPDYITGGNSCHFGKQYTSWRTYIMVNATNMGSSFSDELVDVTVYIQVDPPLLE 132
QY 244 VHSVRVGGLEDQLSVRWV--SPALKDF---LPQAKYQIRYRVSDVWKVDDVSNQTS 298
DB 133 LAV-EVKQPEDRKPYLWIKWSPTLIDLKTGWFTLLYIRLKPKEAAWE-IHFAQQOTE 190
QY 299 CRLAGLKPGTVFVQVRCNPFGLYGSKKAGIWSWSHPTAASPSE 345
DB 191 FKTLSLHPGQKYLQVQRCKP-----DHGYWSAWSPATFIQIPSGD 230

RESULT 12
Q96P36 HUMAN
ID Q96P36_HUMAN PRELIMINARY; PRT; 288 AA.
AC Q96P36;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prolactin receptor short isoform 1b.
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC HOMO
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=placenta;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX Hu Z.Z., Meng J., Dufau M.L.;
RA PubMed=11518703;
RT "Isolation and characterization of two novel forms of the human
RT prolactin receptor generated by alternative splicing of a newly
RT identified exon 11."

RL J. Biol. Chem. 276:41086-41094 (2001).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AF416618; AAL23914.1; -; mRNA.
DR PIR; B59405; B59405.
DR HSSP; P16471; 1BP3.
DR SMR; Q96P36; 29-227.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; HemptreceptL_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS0853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 288 AA; 32760 MW; B45203EC045EB417 CRC64;
Query Match 14.7%; Score 331; DB 2; Length 288;
Best Local Similarity 37.5%; Pred. No. 6e-18;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;
QY 126 ILAGSCLYVG-LPPEKPFNISCWSNMKDLTCRWTPGAHGETFLHNTYSLKYKLRWYGD 184
DB 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTYHREGETLM 72
QY 185 NTCEEYHTVGHPSCHIPKD-LALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDPPPD 243
DB 73 HCEPDYITGGNSCHFGKQYTSWRTYIMVNATNMGSSFSDELVDVTVYIQVDPPLLE 132
QY 244 VHSVRVGGLEDQLSVRWV--SPALKDF---LPQAKYQIRYRVSDVWKVDDVSNQTS 298
DB 133 LAV-EVKQPEDRKPYLWIKWSPTLIDLKTGWFTLLYIRLKPKEAAWE-IHFAQQOTE 190
QY 299 CRLAGLKPGTVFVQVRCNPFGLYGSKKAGIWSWSHPTAASP 342
DB 191 FKTLSLHPGQKYLQVQRCKP-----DHGYWSAWSPATFIQIP 227
RESULT 13
Q9UHJ5 HUMAN
ID Q9UHJ5_HUMAN PRELIMINARY; PRT; 349 AA.
AC Q9UHJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Intermediate prolactin receptor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC HOMO
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20054419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
RT prolactin receptor."
RL J. Biol. Chem. 274:35461-35468 (1999).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AF166329; AAD49855.1; -; mRNA.
DR HSSP; P16471; 1BP3.
DR SMR; Q9UHJ5; 29-227.
GO; GO:0009986; C:cell surface; IDA.

```
DR GO:0042978; F:ornithine decarboxylase activator activity; NAS.
DR GO:0004925; F:prolactin receptor activity; NAS.
DR GO:0042803; F:protein homodimerization activity; NAS.
DR GO:0006916; P:anti-apoptosis; NAS.
DR GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.
DR GO:0007595; P:lactation; NAS.
DR GO:0008694; P:steroid biosynthesis; NAS.
DR GO:0042110; P:T-cell activation; NAS.
DR GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
DR GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS.
DR InterPro: IPR002996; Cyclic_nucept_B/G.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; HemptreceptL_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS50853; FN3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 349 AA; 39806 MW; 932F200E850CDD27 CRC64;

Query Match 14.7%; Score 331; DB 2; Length 349;
Best Local Similarity 37.5%; Pred. No. 7.7e-18;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLVYG-LPPEKPFNISCWSNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQGD 184
Db 15 LFLNTCLLGLQPLPGKPIFKCRSPKETFCTWRPGTDGG--LPTNYSLYVHREGETLM 72
QY 185 NTCEYHTVGHSHCHPKD-LALFTPEIWEATNRLGARSDDLTLVDLVVTTDPPDP 243
Db 73 HECPDYITGGPNSCHFGKQYTSMTYIMMNVNATNMGSSFSDELYVDVTVIVQDPDPLE 132
QY 244 VHVSRVGGLEDQLSVRWV--SPALKDQF---LFOAKYQIRYRVDSVDMKVDDVSNOTS 298
Db 133 LAV-EVKQPEDRKPYLMIKWSPPTLIDLTGWFTLLYELRLKPEKAAWE-IHFAGQOTE 190
QY 299 CRLAGLKPGTVYFVQVRCNPFGIYKSKAGIWSHPTAASTP 342
Db 191 FKILSLHFGQKYLQVRCKP-----DHGYWSAWSPATFIQIP 227

RESULT 14
Q96P35 HUMAN PRELIMINARY; PRT; 376 AA.
AC Q96P35.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Prolactin receptor short isoform 1a.
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=11518703;
RA Hu Z.-Z., Meng J., Dufau M.L.;
RT "Isolation and characterization of two novel forms of the human
RT prolactin receptor generated by alternative splicing of a newly
RT identified exon 11."
RL J. Biol. Chem. 276:41086-41094(2001).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
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DR EMBL; AF416619; AAL23915.1; -; mRNA.
DR PIR; A59405; A59405.
DR HSSP; P16471; 1BP3.
DR SMR; Q96P35; 29-227.
DR Ensembl; ENSG00000113494; Homo sapiens.
DR GO:0009986; C:cell surface; ISS.
DR GO:0042978; F:ornithine decarboxylase activator activity; ISS.
DR GO:0004925; F:prolactin receptor activity; ISS.
DR GO:0042803; F:protein homodimerization activity; ISS.
DR GO:0006916; P:anti-apoptosis; ISS.
DR GO:0007166; P:cell surface receptor linked signal transdu. . .; ISS.
DR GO:0007595; P:lactation; ISS.
DR GO:0008694; P:steroid biosynthesis; ISS.
DR GO:0042110; P:T-cell activation; ISS.
DR GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR GO:0042977; P:tyrosine phosphorylation of JAK2 protein; ISS.
DR InterPro: IPR002996; Cyclic_nucept_B/G.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; HemptreceptL_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS50853; FN3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 376 AA; 42639 MW; 112DC3555FBC4601 CRC64;

Query Match 14.7%; Score 331; DB 2; Length 376;
Best Local Similarity 37.5%; Pred. No. 8.4e-18;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLVYG-LPPEKPFNISCWSNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQGD 184
Db 15 LFLNTCLLGLQPLPGKPIFKCRSPKETFCTWRPGTDGG--LPTNYSLYVHREGETLM 72
QY 185 NTCEYHTVGHSHCHPKD-LALFTPEIWEATNRLGARSDDLTLVDLVVTTDPPDP 243
Db 73 HECPDYITGGPNSCHFGKQYTSMTYIMMNVNATNMGSSFSDELYVDVTVIVQDPDPLE 132
QY 244 VHVSRVGGLEDQLSVRWV--SPALKDQF---LFOAKYQIRYRVDSVDMKVDDVSNOTS 298
Db 133 LAV-EVKQPEDRKPYLMIKWSPPTLIDLTGWFTLLYELRLKPEKAAWE-IHFAGQOTE 190
QY 299 CRLAGLKPGTVYFVQVRCNPFGIYKSKAGIWSHPTAASTP 342
Db 191 FKILSLHFGQKYLQVRCKP-----DHGYWSAWSPATFIQIP 227

RESULT 15
PRLR HUMAN
ID PRLR HUMAN STANDARD; PRT; 622 AA.
AC P16471; Q16354; Q9BX87;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=90114212; PubMed=2558309;
RA Boutin J.-M., Edery M., Shiota M., Jolicoeur C., Lesueur L., Ali S.,
RA Gould D., Djane J., Kelly P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells."
RL Mol. Endocrinol. 3:1455-1461(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;
RA Hu Z.-Z., Zhuang L., Meng J., Leondires M., Dufau M.L.;
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RT "The human prolactin receptor gene structure and alternative promoter
RT utilization: the generic promoter hP111 and a novel human promoter
RT hP(N).";
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Mammary carcinoma;
RA Kline J.B., Cleveland C.V.;
RT "Characterization of a novel and functional human prolactin receptor
RT isoform (delta-S1 PRLr) containing only one extracellular fibronectin-
RT like domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Placenta;
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hellon E., Kettman A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).
RC TISSUE=Mammary carcinoma;
RX MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;
RA Fuh G., Wells J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
RT cancer cell lines.";
RL J. Biol. Chem. 270:13133-13137(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
RX MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;
RA Somers W., Ulteich M., de Vos A.M., Kossiakoff A.A.;
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";
RL Nature 372:478-481(1994).
CC -|- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.
CC -|- INTERACTION:
CC P51956:NEK3; NbExp=1; IntAct=EBI-476182, EBI-476041;
CC P52735:VAV2; NbExp=1; IntAct=EBI-476182, EBI-297549;
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P16471-1; Sequence=Displayed;
CC Name=2; Synonyms=Delta-S1;
CC IsoId=P16471-2; Sequence=VSP_001720;
CC Name=3;
CC IsoId=P16471-3; Sequence=VSP_012620, VSP_012621;
CC Note=Soluble isoform that appears specific for the BT-474 breast
CC cancer cell line;
CC -|- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -|- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -|- SIMILARITY: Belongs to the type I cytokine receptor family. Type 1
CC subfamily.

CC CC -|- SIMILARITY: Contains 2 fibronectin type-III domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M31661; AAA60174.1; -; mRNA.
CC EMBL; AF091870; AAD32032.1; -; Genomic DNA.
CC EMBL; AF091863; AAD32032.1; JOINED; Genomic DNA.
CC EMBL; AF091864; AAD32032.1; JOINED; Genomic DNA.
CC EMBL; AF091865; AAD32032.1; JOINED; Genomic DNA.
CC EMBL; AF091866; AAD32032.1; JOINED; Genomic DNA.
CC EMBL; AF091867; AAD32032.1; JOINED; Genomic DNA.
CC EMBL; AF091868; AAD32032.1; JOINED; Genomic DNA.
CC EMBL; AF091869; AAD32032.1; JOINED; Genomic DNA.
CC EMBL; AF349939; AAK32703.1; -; mRNA.
CC EMBL; BC059392; AAHS9392.1; -; mRNA.
CC EMBL; S78505; AAB34470.1; -; mRNA.
CC PIR; A40144; A40144.
CC PDB; 1BP3; X-ray; B=25-235.
CC IntAct; P16471; -;
CC Ensembl; ENSG00000113494; Homo sapiens.
CC HGNC; HGNC:9446; PRLR.
CC MIM; 176761; -;
CC GO; GO:0009986; C:cell surface; IDA.
CC GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.
CC GO; GO:0004925; F:prolactin receptor activity; NAS.
CC GO; GO:0042803; F:protein homodimerization activity; NAS.
CC GO; GO:0006936; F:anti-apoptosis; NAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; NAS.
CC GO; GO:0007566; P:embryo implantation; TAS.
CC GO; GO:0007595; P:lactation; NAS.
CC GO; GO:0006694; P:steroid biosynthesis; NAS.
CC GO; GO:0042110; P:T cell activation; NAS.
CC GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; IDA.
CC GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS.
CC InterPro; IPR002996; Cytokn_recept_B/G.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; HemptreceptL_F1.
CC Pfam; PF00041; fn3; 2.
CC PROSITE; PS50853; FN3; 2.
CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
CC 3D-structure; Alternative splicing; Glycoprotein; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 622
FT TOPO_DOM 25 234
FT TRANSMEM 235 258
FT TOPO_DOM 259 622
FT DOMAIN 27 121
FT DOMAIN 127 227
FT MOTIF 215 219
FT MOTIF 267 275
FT CARBOHYD 59 59
FT CARBOHYD 104 104
FT CARBOHYD 233 233
FT DISULFID 36 46
FT DISULFID 75 86
FT VARSPPLIC 24 124
FT VARSPPLIC 229 230
FT VARSPPLIC 231 622
FT STRAND 31 38
FT STRAND 44 50
FT STRAND 61 66
FT STRAND 73 74
FT TURN 80 81
FT STRAND 85 88
FT TURN 91 92

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Result No.	Quality			DB	ID	Description
	Score	Match	Length			
1	2197.5	97.6	425	2	US-09-071-224-6	Sequence 6, Appli
2	2119.5	94.1	407	2	US-09-521-335-13	Sequence 13, Appli
3	2118.5	94.1	405	2	US-09-012-072-2	Sequence 2, Appli
4	2118.5	94.1	405	2	US-09-120-601-2	Sequence 2, Appli
5	2114.5	93.9	410	2	US-09-521-335-12	Sequence 12, Appli
6	2098	93.2	425	2	US-09-071-224-4	Sequence 4, Appli
7	2096	93.1	422	2	US-09-866-028-32	Sequence 32, Appli
8	2096	93.1	422	2	US-09-944-457-32	Sequence 32, Appli
9	2096	93.1	422	2	US-09-945-584-32	Sequence 32, Appli
10	2096	93.1	422	2	US-09-944-944-32	Sequence 32, Appli
11	2096	93.1	422	2	US-09-945-587-32	Sequence 32, Appli
12	2092	92.9	422	2	US-09-071-224-2	Sequence 2, Appli
13	2075.5	92.2	448	2	US-09-120-601-6	Sequence 6, Appli
14	2015.5	89.5	434	2	US-09-012-072-4	Sequence 4, Appli
15	2015.5	89.5	434	2	US-09-120-601-4	Sequence 4, Appli
16	2006.5	89.1	385	2	US-09-071-224-19	Sequence 19, Appli
17	1982	88.0	392	2	US-09-071-224-18	Sequence 18, Appli
18	1970.5	87.5	388	2	US-09-071-224-17	Sequence 17, Appli
19	1967	87.4	389	2	US-09-071-224-28	Sequence 28, Appli
20	1966	87.3	389	2	US-09-071-224-22	Sequence 22, Appli
21	1965	87.3	389	2	US-09-071-224-29	Sequence 29, Appli
22	1964	87.2	389	2	US-09-071-224-30	Sequence 30, Appli
23	1963	87.2	389	2	US-09-071-224-24	Sequence 24, Appli
24	1963	87.2	389	2	US-09-071-224-25	Sequence 25, Appli
25	1963	87.2	389	2	US-09-071-224-27	Sequence 27, Appli
26	1962	87.1	389	2	US-09-071-224-26	Sequence 26, Appli
27	1961	87.1	389	2	US-09-071-224-31	Sequence 31, Appli

Query Match 97.6%; Score 2197.5; DB 2; Length 425;
Best Local Similarity 97.6%; Pred. No. 4.4e-197;
Matches 404; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 1 MPAGRGVPAQSNRRPRPLSSLSWSPALLCVLGVPRGGGAHTAVISPODPTLLIGSSLO 60
DB 1 MPAGGPGAAQARRPRRLSSLSWSPALLCVLGVPRGGGAHTAVISPODPTLLIGSSLO 60

QY 61 ATCSIHGDTPGAETAEGLYWTNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 61 ATCSIHGDTPGAETAEGLYWTNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
DB 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180

QY 181 YGQDNTCEEYHTVGPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240
DB 181 YGQDNTCEEYHTVGPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240

QY 241 PPDVHVSVRVGGLEDQLSVRWSPALCKDFLFOAKYQIRYRVSDVWKVDDVSNQTSCK 300
DB 241 PPDVHVSVRVGGLEDQLSVRWSPALCKDFLFOAKYQIRYRVSDVWKVDDVSNQTSCK 300

QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGE 360
DB 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGE 360

QY 361 PSSGPPVRRRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQSKHTRNQ---VLPA 411
DB 361 PSSGPPVRRRELKQFLGMLKKHAYCSNLSFRLYDQWRAMQSKHTRNQDEGILPS 414

RESULT 2
US-09-521-335-13
; Sequence 13, Application US/09521335
; Patent No. 6800460
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/09/521,335
; CURRENT FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-09-521-335-13

Query Match 94.1%; Score 2119; DB 2; Length 407;
Best Local Similarity 98.5%; Pred. No. 9.2e-190;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

QY 18 RPLSSLSWSPALLCVLGVPRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGAETAEGL 77
DB 1 RPLSSLSWSPALLCVLGVPRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGAETAEGL 60

QY 78 YWTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLP 137
DB 61 YWTLNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLP 119

QY 138 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEEYHTVGPSS 197
DB 120 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEEYHTVGPSS 179

QY 198 CHPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPDVHVSVRVGGLEDQLS 257

DB 180 CHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPDVHVSVRVGGLEDQLS 239

QY 258 VRWVSPALKDPLFOAKYQIRYRVSDVWKVDDVSNQTSCLRLAGLKPGTVYFVQVRCN 317
DB 240 VRWVSPALKDPLFOAKYQIRYRVSDVWKVDDVSNQTSCLRLAGLKPGTVYFVQVRCN 299

QY 318 PFGIYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWL 377
DB 300 PFGIYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWL 359

QY 378 KKHAYCSNLSFRLYDQWRAMQSKHTRNQ---VLPA 411
DB 360 KKHAYCSNLSFRLYDQWRAMQSKHTRNQDEGILPS 396

RESULT 3
US-09-012-072-2
; Sequence 2, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiaowski, Piotr
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-012-072-2

Query Match 94.1%; Score 2118.5; DB 2; Length 405;
Best Local Similarity 98.7%; Pred. No. 1e-189;
Matches 389; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 21 SSLWSPLLLCVLGVPRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGAETAEGLYWT 80
DB 1 SSLWSPLLLCVLGVPRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGAETAEGLYWT 60

QY 81 LNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 140
DB 61 LNGRRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 120

QY 141 PFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEEYHTVGPSSCHI 200
DB 121 PFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEEYHTVGPSSCHI 180

QY 201 PKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPDVHVSVRVGGLEDQLSVRW 260
DB 181 PKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDPDPDVHVSVRVGGLEDQLSVRW 240

QY 261 VSPALKDPLFOAKYQIRYRVSDVWKVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPF 320
DB 241 VSPALKDPLFOAKYQIRYRVSDVWKVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPF 300

QY 321 IYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGMLKKH 380
DB 301 IYGSKKAGIWESEWSPHTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGMLKKH 360

QY 381 AYCNSLSFRLYDQWRAMQSKHTRNQ---VLPA 411
DB 361 AYCNSLSFRLYDQWRAMQSKHTRNQDEGILPS 394

RESULT 4
US-09-120-601-2
; Sequence 2, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masiaowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors

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; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-120-601-2

Query Match          94.1%; Score 2118.5; DB 2; Length 405;
Best Local Similarity 98.7%; Pred. No. 1e-189;
Matches 389; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 21 SSIWSPLLLCVLGVRPGSGGANTAVISPDPTLLIGSSLOATCSIHGDTPGATAGLYWT 80
DB 1 SSIWSPLLLCVLGVRPGSGGANTAVISPDPTLLIGSSLOATCSIHGDTPGATAGLYWT 60
QY 81 LNRRLPSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEK 140
DB 61 LNRRLPSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEK 120
QY 141 PFNISCWSRNKMDLTCRWTPGAGHETFLHTNYSKYKLAWYQDNTCEEYHTVGPSC 200
DB 121 PFNISCWSRNKMDLTCRWTPGAGHETFLHTNYSKYKLAWYQDNTCEEYHTVGPSC 180
QY 201 PKDLALFTPEYIWEATNRLGARSDDLTLVDLVDTTDPDVRVSVRGGLDQLSVRW 260
DB 181 PKDLALFTPEYIWEATNRLGARSDDLTLVDLVDTTDPDVRVSVRGGLDQLSVRW 240
QY 261 VSPPALKDFLQKQIRYRVSDSVDMKVVDVDSNQTSLAGLKPQTVYFVQVRCNPRG 320
DB 241 VSPPALKDFLQKQIRYRVSDSVDMKVVDVDSNQTSLAGLKPQTVYFVQVRCNPRG 300
QY 321 IYSGKAGIWSHPTAASTPRSRPGGVCBPRGSGGVRRELKQFLGWLKXH 380
DB 301 IYSGKAGIWSHPTAASTPRSRPGGVCBPRGSGGVRRELKQFLGWLKXH 360
QY 381 AYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA 411
DB 361 AYCSNLSFRLYDQWRAWMQKSHKTRNQDEGLIPS 394

RESULT 5
US-09-521-335-12
; Sequence 12, Application US/09521335
; Patent No. 6800460
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/09/521,335
; CURRENT FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 410
; TYPE: PRT
; ORGANISM: primate
US-09-521-335-12

Query Match          93.9%; Score 2114.5; DB 2; Length 410;
Best Local Similarity 94.7%; Pred. No. 2.5e-189;
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRRGPVAGSARRPPPLSLWSPLLLCVLGVRPGSGGANTAVISPDPTLLIGSS 60
DB 1 MPAGRRGPVAGSARRPPPLSLWSPLLLCVLGVRPGSGGANTAVISPDPTLLIGSS 57
QY 61 ATCSIHGDTPGATAGLYWTINLGRRLPSELSRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDPGATAGLYWTINLGRRLPSELSRLNTSTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAGHETFLHTNYSKYKL 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAGHETFLHTNYSKYKL 177
QY 181 YQDNTCEEYHTVGPSCHPKDLALFTPEYIWEATNRLGARSDDLTLVDLVDTTDP 240
DB 178 YQDNTCEEYHTVGPSCHPKDLALFTPEYIWEATNRLGARSDDLTLVDLVDTTDP 237
QY 241 PDVHVSVRVGGLEDQLSVRWSPPALKDFLQKQIRYRVSDSVDMKVVDVDSNQTSCR 300
DB 238 PDVHVSVRVGGLEDQLSVRWSPPALKDFLQKQIRYRVSDSVDMKVVDVDSNQTSCR 297
QY 301 LAGLKPQTVYFVQVRCNPRPGIYSGKAGIWSHPTAASTPRSRPGGVCBPRGSG 360
DB 298 LAGLKPQTVYFVQVRCNPRPGIYSGKAGIWSHPTAASTPRSRPGGVCBPRGSG 357
QY 361 PSSGVRRELKQFLGWLKXHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPAKL 413
DB 358 PSSGVRRELKQFLGWLKXHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPAKL 410

RESULT 6
US-09-071-224-4
; Sequence 4, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-4

Query Match      93.2%; Score 2098; DB 2; Length 425;
Best Local Similarity 91.1%; Pred. No. 9,1e-188;
Matches 391; Conservative 5; Mismatches 13; Indels 20; Gaps 3;

QY 1 MPAGRPGVAQASARRPPPLSLWSPLLLCVLGVPRGSGAHTAVISQDPTLLIGSSILQ 60
DB 1 MPAGRRGPAQASARRPP-PLLP-LL-LLLCVLGAPRAGSGAHTAVISQDPTLLIGSSIL 56
QY 61 ATCSITHGDTPGATAGLWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 57 ATCSVHGDPGATAGLWTLNGRLPPELSRVINASTLALANLNGSRQSGDNLVCH 116
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 117 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 176
QY 181 YQDNTCEYHTVGVPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 240
DB 177 YQDNTCEYHTVGVPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 236
QY 241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300
DB 237 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 296
QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSERPGGGVCBPRGGE 360
DB 297 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSERPGGGVCBPRGGE 356
QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQ----- 407
DB 357 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQADGA 416
QY 408 --VLPAKL 413
DB 417 RREVLPDKL 425

RESULT 7
US-09-866-028-32
; Sequence 32, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425

;
; ORGANISM: Homo Sapien
US-09-866-028-32

Query Match      93.1%; Score 2096; DB 2; Length 422;
Best Local Similarity 93.7%; Pred. No. 1.4e-187;
Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPGVAQASARRPPPLSLWSPLLLCVLGVPRGSGAHTAVISQDPTLLIGSSILQ 60
DB 1 MPAGRRGPAQASARRPP-PLLP-LL-LLLCVLGAPRAGSGAHTAVISQDPTLLIGSSIL 57
QY 61 ATCSITHGDTPGATAGLWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDPGATAGLWTLNGRLPPELSRVINASTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177
QY 181 YQDNTCEYHTVGVPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 240
DB 178 YQDNTCEYHTVGVPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLVDLVVTTDP 237
QY 241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300
DB 238 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 297
QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSERPGGGVCBPRGGE 360
DB 298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSBWSHPTAASPRSERPGGGVCBPRGGE 357
QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQ---VLPA 411
DB 358 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPS 411

RESULT 8
US-09-944-457-32
; Sequence 32, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
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, PRIOR FILING DATE: December 12, 1997
, PRIOR APPLICATION NUMBER: 60/069,696
, PRIOR FILING DATE: December 16, 1997
, PRIOR APPLICATION NUMBER: 60/069,694
, PRIOR FILING DATE: December 16, 1997
, PRIOR APPLICATION NUMBER: 60/069,702
, PRIOR FILING DATE: December 16, 1997
, PRIOR APPLICATION NUMBER: 60/069,870
, PRIOR FILING DATE: December 17, 1997
, PRIOR APPLICATION NUMBER: 60/069,873
, PRIOR FILING DATE: December 17, 1997
, PRIOR APPLICATION NUMBER: 60/068,017
, PRIOR FILING DATE: December 18, 1997
, PRIOR APPLICATION NUMBER: 60/070,440
, PRIOR FILING DATE: January 5, 1998
, PRIOR APPLICATION NUMBER: 60/074,086
, PRIOR FILING DATE: February 9, 1998
, PRIOR APPLICATION NUMBER: 60/074,092
, PRIOR FILING DATE: February 9, 1998
, PRIOR APPLICATION NUMBER: 60/075,945
, PRIOR FILING DATE: February 25, 1998
, PRIOR APPLICATION NUMBER: 60/113,850
, PRIOR FILING DATE: December 16, 1998
, PRIOR APPLICATION NUMBER: 60/113,296
, PRIOR FILING DATE: December 22, 1998
, PRIOR APPLICATION NUMBER: 60/146,222
, PRIOR FILING DATE: July 28, 1999
, PRIOR APPLICATION NUMBER: PCT/US98/19330
, PRIOR FILING DATE: September 16, 1998
, PRIOR APPLICATION NUMBER: PCT/US98/25108
, PRIOR FILING DATE: December 1, 1998
, PRIOR APPLICATION NUMBER: 09/216,021
, PRIOR FILING DATE: December 16, 1998
, PRIOR APPLICATION NUMBER: 09/218,517
, PRIOR FILING DATE: December 22, 1998
, PRIOR APPLICATION NUMBER: 09/254,311
, PRIOR FILING DATE: March 3, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/12252
, PRIOR FILING DATE: June 22, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/21090
, PRIOR FILING DATE: September 15, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/28409
, PRIOR FILING DATE: No. 6734288ember 30, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/28313
, PRIOR FILING DATE: No. 6734288ember 30, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/28301
, PRIOR FILING DATE: December 1, 1999
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: December 16, 1999
, PRIOR APPLICATION NUMBER: PCT/US00/03565
, PRIOR FILING DATE: February 11, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/04414
, PRIOR FILING DATE: February 22, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/05841
, PRIOR FILING DATE: March 2, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/08439
, PRIOR FILING DATE: March 30, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/14042
, PRIOR FILING DATE: May 22, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/20710
, PRIOR FILING DATE: July 28, 2000
, PRIOR APPLICATION NUMBER: PCT/US00/32678
, PRIOR FILING DATE: December 1, 2000
, PRIOR APPLICATION NUMBER: PCT/US01/06520
, PRIOR FILING DATE: February 28, 2001
, NUMBER OF SEQ ID NOS: 120
, SEQ ID NO 32
, LENGTH: 422
, TYPE: PRT
, ORGANISM: Homo Sapien
, US-09-944-457-32

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Query Match 93.1%; Score 2096; DB 2; Length 422;

Best Local Similarity	93.7%;	Pred. No. 1.4e-197;							
Matches	386;	Conservative	7;	Mismatches	13;	Indels	6;	Gaps	3;
Qy	1	MPAGRPQVQAQARRPPRLPSLLSPULLCVLGVPRGSGGAHTAVISPDPTLLIGSSLQ	60						
Db	1	MPAGRGPAQAQARRPP-FLPPLL--LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSL	57						
Qy	61	ATCSIIHGDTPGAVAGLYWTLNGRRLPSELSSRLNTSTLALANLNGSRQSGDNLVCH	120						
Db	58	ATCSVHGDDPGATAEGLYWTLNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCH	117						
Qy	121	ARDGSILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAGGETPLHTNYSLYKYLKW	180						
Db	118	ARDGSILAGSCLYVGLPPEKPFVNISCWSKNKMDLTCRWTPGAGGETPLHTNYSLYKYLKW	177						
Qy	181	YGQDNTCEEVHTVGHSHCHTPKOLALPTPYEIVWEATNRLGARSQSVLTLDVLDDVVTDP	240						
Db	178	YGQDNTCEEVHTVGHSHCHTPKOLALFTPYEIVWEATNRLGARSQSVLTLDVLDDVVTDP	237						
Qy	241	PPDVHVSRVGGLDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVDDVSNQTSR	300						
Db	238	PPDVHVSRVGGLDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVDDVSNQTSR	297						
Qy	301	LAKLPGCTVYFVQVRNCPFGIYGSKKAGIWEKSHPTAASTPRSRPGCGVCEPRGGE	360						
Db	298	LAKLPGCTVYFVQVRNCPFGIYGSKKAGIWEKSHPTAASTPRSRPGCGGACEPRGGE	357						
Qy	361	PSSGPRRELKQFLGWLKHAHCNSLSFRLYDQWRAMMQKSHKTRNQ---VLPA	411						
Db	358	PSSGPRRELKQFLGWLKHAHCNSLSFRLYDQWRAMMQKSHKTRNDEGLPS	411						

RESULT 9

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US-09-945-584-32
; Sequence 32, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Hurren, Austen
; APPLICANT: Gillan, Kenneth
; APPLICANT: KJavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRAN
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2549P1C1
; CURRENT APPLICATION NUMBER: US/09/945.584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694

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PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. 6908993ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. 6908993ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 32
 LENGTH: 422
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-945-584-32

Query Match 93.1%; Score 2096; DB 2; Length 422;
 Best Local Similarity 93.7%; Pred. No. 1.4e-187;
 Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;
 1 MPACRGPAAQARRPP-PLLP--LLLCVLPAGRAGSAGHTAVISPDPTLLIGSSIL 60

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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 692994/ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 692994/ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-944-32

Query Match          93.1%; Score 2096; DB 2; Length 422;
Best Local Similarity 93.7%; Pred. No. 1.4e-187;
Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPGPVAQARRPPRLSSLSWSPLLCLVLPVPRGSGGAHTAVISPODPTLLIGSSLQ 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MPAGRGPAAQARRPP-PULPLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ATCSIHGDTFGATAEGLYWTNGRRLLPSELSRLNTSTLALANLNGSRQSGDNLVCH 120
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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
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; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
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; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
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; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 692994/ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 692994/ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-944-32

; Db 58 ATCSVHGDPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117
; QY 121 ARDGSILAGSCLVGLPPEKPFNISCSNRNMKDLTCRWTPGAHGETPLHTNYSLSKYLRLW 180
; Db 118 ARDGSILAGSCLVGLPPEKPFVNISCSNMKDLTCRWTPGAHGETPLHTNYSLSKYLRLW 177
; QY 181 YGQDNTCEEYHTVGPCHSCHIPKDLALFTPYEIVWEATNRLGSARSVDLTLDVLDVVTDP 240
; Db 178 YGQDNTCEEYHTVGPCHSCHIPKDLALFTPYEIVWEATNRLGSARSVDLTLDVLDVVTDP 237
; QY 241 PPDVHVSRVGGLDQLSVRWVSPALKDFLFQAKYQIRYRVESVDMKVVDVDSNQTSCR 300
; Db 238 PPDVHVSRVGGLDQLSVRWVSPALKDFLFQAKYQIRYRVESVDMKVVDVDSNQTSCR 297
; QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASTPRSERPGGVCERPGGE 360
; Db 298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWESESHPTAASTPRSERPGGVCERPGGE 357
; QY 361 PSSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSKHTRNQ---VLPA 411
; Db 358 PSSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSKHTRNQDGEILPS 411

RESULT 11
US-09-945-587-32
; Sequence 32, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR APPLICATION NUMBER: 60/068,017
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; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
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; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-32

Query Match          93.1%; Score 2096; DB 2; Length 422;
Best Local Similarity 93.7%; Pred. No. 1.4e-187;
Matches 388; Conservative 7; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRGPGVQAQARRPPRLSSLLWSPVLLVLPVGGGGAHTAVISPDPTLLIGSSLQ 60
    |||||
DB 1 MPAGRGPGVQAQARRPP-PLLP-LL-LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSL 57
    |||||

QY 61 ATCSIHGDTFGATAEGLYWTNGRRRLPSRLNTSTLALANLNGSRQQSGDNLVCH 120
    |||||
DB 58 ATCSVHGDPGATAEGLYWTNGRRRLPSRLNASTLALANLNGSRQRSGDNLVCH 117
    |||||

QY 121 ARDGSILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTGAGHETFLHTNYSILKYLRW 180
    |||||
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Db 118 ARDGSILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTGAGHETFLHTNYSILKYLRW 177
    |||||
QY 181 YQODNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLFLDLDVVTDDP 240
    |||||
DB 178 YQODNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLFLDLDVVTDDP 237
    |||||
QY 241 PPDVHVSRYVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNOTSCR 300
    |||||
DB 238 PPDVHVSRYVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNOTSCR 297
    |||||
QY 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGGGGVCEPRGGG 360
    |||||
DB 298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGGGGVCEPRGGG 357
    |||||
QY 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQ---VLP 411
    |||||
DB 358 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPS 411
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RESULT 12
US-09-071-224-2
; Sequence 2, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-2

Query Match          92.9%; Score 2092; DB 2; Length 422;
Best Local Similarity 93.5%; Pred. No. 3.3e-187;
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Matches 387; Conservative 8; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPGPVAQARRPPRLSSLSWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSILQ 60

Db 1 MPAGRRGPAAQARRPP-PLLP--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57

QY 61 ATCSIHGDPGATAGLYTLNGRRLLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120

Db 58 ATCSVHGDPGATAGLYTLNGRRLLPSLSRLNTSTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180

Db 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 177

QY 181 YGQDNTCEBYHTVGPHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDLVVTTDP 240

Db 178 YGQDNTCEBYHTVGPHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDLVVTTDP 237

QY 241 PDVHVSRVGGLEDQLSVRWSPALKDPLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300

Db 238 PPEVHVSRRVGGLEDQLSVRWSPALKDPLFOAKYQIRYRVEDSVWKVDDVSNQTSR 297

QY 301 LAGLKPGTVFVQVRCNPGIYSGKKAGIWSKSHPTAASTPRSRPGGVCERGG 360

Db 298 LAGLKPGTVFVQVRCNPGIYSGKKAGIWSKSHPTAASTPRSRPGGVCERGG 357

QY 361 PSSGPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLPA 411

Db 358 PSSGPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS 411

RESULT 13

US-09-120-601-6

; Sequence 6, Application US/09120601

; Patent No. 6207413

; GENERAL INFORMATION:

; APPLICANT: Masiaowski, Piotr

; TITLE OF INVENTION: No. 6207413el Orphan Receptors

; FILE REFERENCE: REG 630

; CURRENT APPLICATION NUMBER: US/09/120,601

; CURRENT FILING DATE: 1998-07-22

; EARLIER APPLICATION NUMBER: 09/012,072

; EARLIER FILING DATE: 1998-01-22

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 448

; TYPE: PRT

; ORGANISM: HUMAN

US-09-120-601-6

Query Match 92.2%; Score 2075.5; DB 2; Length 448;

Best Local Similarity 86.7%; Pred. No. 1.2e-185;

Matches 391; Conservative 5; Mismatches 14; Indels 41; Gaps 4;

QY 1 MPAGRPGPVAQARRPPRLSSLSWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSILQ 60

Db 1 MPAGRRGPAAQARRPP-PLLP--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57

QY 61 ATCSIHGDPGATAGLYTLNGRRLLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120

Db 58 ATCSVHGDPGATAGLYTLNGRRLLPSLSRLNTSTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180

Db 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 177

Db 238 LPSPATPGLSVLVRGKVTTDPPDVHVSRRVGGLEDQLSVRWVSPPALKDPLFOAKYQIR 297

QY 279 YRVEDSVWKVDDVSNQTSCLAGLKPGTVFVQVRCNPFPGIYSGKKAGIWSKSHPTA 338

Db 298 YRVEDSVWKVDDVSNQTSCLAGLKPGTVFVQVRCNPFPGIYSGKKAGIWSKSHPTA 357

QY 339 ASTPRSRPGGVCERPGGSPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMW 398

Db 358 ASTPRSRPGGVCERPGGSPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMW 417

QY 399 QXSHKTRNQ-----VLPAKL 413

Db 418 QXSHKTRNQHRRTRGSCPRADGARREVLPDKL 448

RESULT 14

US-09-012-072-4

; Sequence 4, Application US/09012072

; Patent No. 6060276

; GENERAL INFORMATION:

; APPLICANT: Masiaowski, Piotr

; TITLE OF INVENTION: No. 6060276el Orphan Receptors

; FILE REFERENCE: REG 630

; CURRENT APPLICATION NUMBER: US/09/012,072

; CURRENT FILING DATE: 1998-01-22

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 434

; TYPE: PRT

; ORGANISM: HUMAN

US-09-012-072-4

Query Match 89.5%; Score 2015.5; DB 2; Length 434;

Best Local Similarity 86.7%; Pred. No. 4.9e-180;

Matches 379; Conservative 5; Mismatches 12; Indels 41; Gaps 4;

QY 15 RPP-PLLP--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATA 57

Db 1 RPP-PLLP--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATA 57

QY 75 EGLYTLNGRRLLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 134

Db 58 EGLYTLNGRRLLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 117

QY 135 GLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGDNTCEBYHTVG 194

Db 118 GLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGDNTCEBYHTVG 177

QY 195 PHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDVLD----- 234

Db 178 PHSCHIPKDIALFTPEIWEATNRLGARSVDLTLDVLDVSHLPLSPATPGLSLVLR 237

QY 235 --VTTDPPDVHVSRRVGGLEDQLSVRWVSPPALKDPLFOAKYQIRYRVEDSVWKVDD 292

Db 238 GRVTTDPPDVHVSRRVGGLEDQLSVRWVSPPALKDPLFOAKYQIRYRVEDSVWKVDD 297

QY 293 VSNQTSCLAGLKPGTVFVQVRCNPFPGIYSGKKAGIWSKSHPTAASTPRSRPGG 352

Db 298 VSNQTSCLAGLKPGTVFVQVRCNPFPGIYSGKKAGIWSKSHPTAASTPRSRPGG 357

QY 353 VCEPRGGSPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ----- 407

Db 358 ACEPRGGSPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ----- 417

QY 408 -----VLPAKL 413

Db 418 SCPRADGARREVLPDKL 434

RESULT 15

US-09-120-601-4

; Sequence 4, Application US/09120601

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; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Maslakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-4

Query Match      89.5%; Score 2015.5; DB 2; Length 434;
Best Local Similarity 86.7%; Pred. No. 4.9e-180;
Matches 379; Conservative 5; Mismatches 12; Indels 41; Gaps 4;

Qy 15 RPRPLSSLSLLCLVLPVPGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATA 74
Db 1 RPP-FLPL--LLLCVLGAPRAGGAHTAVISPODPTLLIGSSLLATCSVHGDPGATA 57

Qy 75 EGLYWTNGRRRLPSELRLINTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 134
Db 58 EGLYWTNGRRRLPSELRLINASTLALANLNGSRQSGDNLVCHARDGSIAGSCLYV 117

Qy 135 GLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQDNTCEEYHTVG 194
Db 118 GLPPEKPNISCSWSNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQDNTCEEYHTVG 177

Qy 195 PHSCHIPKDIALFTPYEIWEATNRLGSARSDVLTLDVLD----- 234
Db 178 PHSCHIPKDIALFTPYEIWEATNRLGSARSDVLTLDLDVGSHPPLSPATPGLSLLVR 237

Qy 235 --VTTTDPDPDVHVSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDD 292
Db 238 GKVVTTDPDPDVHVSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDD 297

Qy 293 VSNQTSCLAGLKPVTYFVQVRCNPFYIGYSGKAGIWSHPTAASPRSERPGPGG 352
Db 298 VSNQTSCLAGLKPVTYFVQVRCNPFYIGYSGKAGIWSHPTAASPRSERPGPGG 357

Qy 353 VCEPRGGEPSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----- 407
Db 358 ACEPRGGEPSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQRTG 417

Qy 408 -----VLPAXL 413
Db 418 SCPRADGARREVLDPKL 434
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Search completed: April 11, 2006, 02:18:59
Job time : 29.5393 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:36:34 ; Search time 96.1152 Seconds
(without alignments)
1795.383 Million cell updates/sec

Title: US-09-037-657-13

Perfect score: 2251

Sequence: 1 MPAGRPGVPAQSARPPRL.....WRAMQKSHKTRNQVLPAKL 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2251	100.0	413	3	US-09-037-657-13
2	2226.5	98.9	425	3	US-09-037-657-15
3	2197.5	97.6	425	3	US-09-880-578-6
4	2119	94.1	407	4	US-10-247-463-5
5	2119	94.1	407	4	US-10-778-002-13
6	2119	94.1	407	5	US-10-777-789-13
7	2119	94.1	407	6	US-11-016-106-5
8	2118.5	94.1	405	3	US-09-736-842-2
9	2118.5	94.1	405	4	US-10-074-901-2
10	2114.5	93.9	410	4	US-10-247-463-4
11	2114.5	93.9	410	4	US-10-778-002-12
12	2114.5	93.9	410	5	US-10-777-789-12
13	2114.5	93.9	410	6	US-11-016-106-4
14	2098	93.2	425	3	US-09-880-578-4
15	2097.5	93.2	421	3	US-09-037-657-44
16	2096.5	93.1	426	4	US-10-056-984-2
17	2096.5	93.1	426	5	US-10-643-009-2
18	2096	93.1	422	3	US-09-866-028-32
19	2096	93.1	422	3	US-09-944-449-32
20	2096	93.1	422	3	US-09-944-457-32
21	2096	93.1	422	3	US-09-944-862-32
22	2096	93.1	422	3	US-09-945-587-32
23	2096	93.1	422	3	US-09-945-015-32
24	2096	93.1	422	3	US-09-944-396-32
25	2096	93.1	422	3	US-09-944-432-32
26	2096	93.1	422	3	US-09-943-762-32
27	2096	93.1	422	3	US-09-944-654-32

28	2096	93.1	422	3	US-09-943-851A-32	Sequence 32, Appl
29	2096	93.1	422	3	US-09-944-413-32	Sequence 32, Appl
30	2096	93.1	422	3	US-09-944-403-32	Sequence 32, Appl
31	2096	93.1	422	3	US-09-944-896-32	Sequence 32, Appl
32	2096	93.1	422	3	US-09-944-944-32	Sequence 32, Appl
33	2096	93.1	422	3	US-09-944-929-32	Sequence 32, Appl
34	2096	93.1	422	3	US-09-944-907-32	Sequence 32, Appl
35	2096	93.1	422	3	US-09-944-884-32	Sequence 32, Appl
36	2096	93.1	422	3	US-09-943-852-32	Sequence 32, Appl
37	2096	93.1	422	3	US-09-943-780-32	Sequence 32, Appl
38	2096	93.1	422	3	US-09-945-584-32	Sequence 32, Appl
39	2096	93.1	422	3	US-09-943-664-32	Sequence 32, Appl
40	2096	93.1	422	4	US-10-125-691-2	Sequence 2, Appl
41	2096	93.1	422	4	US-10-429-667-32	Sequence 32, Appl
42	2096	93.1	422	4	US-10-677-471-32	Sequence 32, Appl
43	2096	93.1	422	4	US-10-677-669-32	Sequence 32, Appl
44	2096	93.1	422	4	US-10-329-056-2	Sequence 2, Appl
45	2096	93.1	422	5	US-10-735-014-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-037-657-13
; Sequence 13, Application US/09037657A
; Patent No. US20020045741A1
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Nicola, Nicolas A.
; APPLICANT: Farley, Allison
; APPLICANT: Wilson, Tracy
; APPLICANT: Zhang, Jian-Guo
; APPLICANT: Alexander, Warren
; APPLICANT: Rakar, Steven
; APPLICANT: Fabri, Louis
; APPLICANT: Kojima, Tetsuo
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Kikuchi, Yasufumi
; APPLICANT: Nash, Andrew
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
; CURRENT APPLICATION NUMBER: US/09/037,657A
; CURRENT FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 08/928,720
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1
US-09-037-657-13

Query Match	100.0%;	Score	2251;	DB	3;	Length	413;
Best Local Similarity	100.0%;	Pred. No.	5e-166;				
Matches	413;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MPAGRPGVPAQSARPPRLSLVGLCVLGVPRGSGAHTAVISPODPTLLIGSSIQ	60				
Db	1	MPAGRPGVPAQSARPPRLSLVGLCVLGVPRGSGAHTAVISPODPTLLIGSSIQ	60				
QY	61	ATCSIHGDTPGTAGELVYTLNGLRRLPSLSRLNTSTLALANLNGSRQSGDNLVCH	120				
Db	61	ATCSIHGDTPGTAGELVYTLNGLRRLPSLSRLNTSTLALANLNGSRQSGDNLVCH	120				
QY	121	ARDGSILAGSCLVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW	180				
Db	121	ARDGSILAGSCLVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW	180				

QY 181 YGQDNTCEHYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLVDLVVTTDP 240
DB 181 YGQDNTCEHYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLVDLVVTTDP 240
QY 241 PPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300
DB 241 PPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300
QY 301 LAGLPGTGVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPGGGVCGPRGGE 360
DB 301 LAGLPGTGVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPGGGVCGPRGGE 360
QY 361 PSSGPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 413
DB 361 PSSGPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNOVLPAKL 413

RESULT 2

US-09-037-657-15
; Sequence 15, Application US/09037657A
; Patent No. US20020045741A1
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Farley, Alison
; APPLICANT: Wilson, Tracy
; APPLICANT: Zhang, Jian-Guo
; APPLICANT: Alexander, Warren
; APPLICANT: Rakar, Steven
; APPLICANT: Fabri, Louis
; APPLICANT: Kojima, Tetsuo
; APPLICANT: Maeda, Masateugu
; APPLICANT: Kikuchi, Yasufumi
; APPLICANT: Nash, Andrew
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; FILE REFERENCE: ENCODING SAME
; CURRENT APPLICATION NUMBER: US/09/037,657A
; CURRENT FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 08/928,720
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Murine NR6.2
US-09-037-657-15

Query Match 98.9%; Score 2226.5; DB 3; Length 425;
Best Local Similarity 98.8%; Pred. No. 4.1e-164;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
QY 1 MPAGRPGPVAQSAARRPRPLSSLSWSPLLCLVGVPRGGGAHTAVISPODPTLLIGSSLQ 60
DB 1 MPAGRPGPVAQSAARRPRPLSSLSWSPLLCLVGVPRGGGAHTAVISPODPTLLIGSSLQ 60
QY 61 ATCSIHGDTFGTAEGLYWTNGRRLLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 61 ATCSIHGDTFGTAEGLYWTNGRRLLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
QY 121 ARDGSILAGSLYVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTYSLKYKLWR 180
DB 121 ARDGSILAGSLYVGLPPEKPFNISCWSRNKDLTCRWTPGAHGETFLHNTYSLKYKLWR 180
QY 181 YGQDNTCEHYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLVDLVVTTDP 240
DB 181 YGQDNTCEHYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSVDLTLVDLVVTTDP 240
QY 241 PPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300

DB 241 PPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSR 300
QY 301 LAGLPGTGVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPGGGVCGPRGGE 360
DB 301 LAGLPGTGVYFVQVRCNPFYIGSKKAGIWSWSHPTAASPRSRPGGGVCGPRGGE 360
QY 361 PSSGPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQ---VLPA 411
DB 361 PSSGPVRRRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 414

RESULT 3

US-09-880-578-6
; Sequence 6, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmsberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-880-578-6

Query Match 97.6%; Score 2197.5; DB 3; Length 425;
Best Local Similarity 97.6%; Pred. No. 7.3e-162;
Matches 404; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
QY 1 MPAGRPGPVAQSAARRPRPLSSLSWSPLLCLVGVPRGGGAHTAVISPODPTLLIGSSLQ 60
DB 1 MPAGRPGPVAQSAARRPRPLSSLSWSPLLCLVGVPRGGGAHTAVISPODPTLLIGSSLH 60
QY 61 ATCSIHGDTFGTAEGLYWTNGRRLLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

Db 61 ATCSIHGDTPGATAGLYWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCH 120
QY 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRW 180
Db 121 ARDGSILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRW 180
QY 181 YGQDNTCEBYHTVGPCHSKIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDP 240
Db 181 YGQDNTCEBYHTVGPCHSKIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDP 240
QY 241 PDVHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCK 300
Db 241 PDVHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCK 300
QY 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGGE 360
Db 301 LAGLKPCTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGGE 360
QY 361 PSSGPVRRBKQPLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411
Db 361 PSSGPVRRBKQPLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 414

RESULT 4

US-10-247-463-5
; Sequence 5, Application US/10247463
; Publication No. US20030082734A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; FILE REFERENCE: DX0992Q
; CURRENT APPLICATION NUMBER: US/10/247,463
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-10-247-463-5

Query Match 94.1%; Score 2119; DB 4; Length 407;
Best Local Similarity 98.5%; Pred. No. 8.5e-156;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;
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Db 1 RPLSLWSPLLLCVIGVPRGSGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGL 60
QY 78 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 137
Db 61 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 119
QY 138 PEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 197
Db 120 PEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 179
QY 198 CHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGGLEDQLS 257
Db 180 CHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGGLEDQLS 239
QY 258 VRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCLAGLKPCTVYFVQVRCN 317
Db 240 VRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCLAGLKPCTVYFVQVRCN 299
QY 318 PEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 197
Db 120 PEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 179
QY 198 CHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGGLEDQLS 257
Db 180 CHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGGLEDQLS 239
QY 258 VRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCLAGLKPCTVYFVQVRCN 317
Db 240 VRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCLAGLKPCTVYFVQVRCN 299
QY 318 PEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 197

Db 300 PFGIYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGSGPVRRRELKQPLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411
Db 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

RESULT 5

US-10-778-002-13
; Sequence 13, Application US/10778002
; Publication No. US20040192891A1
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/10/778,002
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/521,335
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-10-778-002-13

Query Match 94.1%; Score 2119; DB 4; Length 407;
Best Local Similarity 98.5%; Pred. No. 8.5e-156;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;
QY 18 RPLSLWSPLLLCVIGVPRGSGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGL 77
Db 1 RPLSLWSPLLLCVIGVPRGSGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGL 60
QY 78 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 137
Db 61 YWTLNGRRLPSELRLNTSTLTALANLNGSRQSGDNLVCHARDGSTLAGSCLYVGLP 119
QY 138 PEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 197
Db 120 PEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPCHS 179
QY 198 CHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGGLEDQLS 257
Db 180 CHIPKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGGLEDQLS 239
QY 258 VRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCLAGLKPCTVYFVQVRCN 317
Db 240 VRWVSPALKDFLFOAKYQIRYRVSDSVKVVDDVSNQTSCLAGLKPCTVYFVQVRCN 299
QY 318 PFGIYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGSGPVRRRELKQPLGWL 377
Db 300 PFGIYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGSGPVRRRELKQPLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411
Db 360 KKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 396

RESULT 6

US-10-777-789-13
; Sequence 13, Application US/10777789
; Publication No. US20050048625A1
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando

```
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/10/777,789
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/521,335
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-10-777-789-13

Query Match          94.1%; Score 2119; DB 5; Length 407;
Best Local Similarity 98.5%; Pred. No. 8.5e-156;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

QY 18 RPLSSLSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGL 77
Db 1 RPLSSLSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGL 60

QY 78 YWTLNGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLP 137
Db 61 YWTLNGRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLP 119

QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLRYWYGDNTCEEYHTVGPHS 197
Db 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLRYWYGDNTCEEYHTVGPHS 179

QY 198 CHIPKDALFTPYEIWEATNRLGSARSDVLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 257
Db 180 CHIPKDALFTPYEIWEATNRLGSARSDVLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 239

QY 258 VRWVSPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 317
Db 240 VRWVSPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 299

QY 318 PFGIYGSKKAGIWSWSHPTAASRPRSGPGGVCPRGSGPVRRELKQFLGWL 377
Db 300 PFGIYGSKKAGIWSWSHPTAASRPRSGPGGVCPRGSGPVRRELKQFLGWL 359

QY 378 KKHAYCSNLSFRLYDQWRAMQSHKTRNQ---VLPA 411
Db 360 KKHAYCSNLSFRLYDQWRAMQSHKTRNQDEGILPS 396

RESULT 7
US-11-016-106-5
; Sequence 5, Application US/11016106
; Publication No. US20050106673A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; FILE REFERENCE: DX0992Q
; CURRENT APPLICATION NUMBER: US/11/016,106
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-11-016-106-5

Query Match          94.1%; Score 2119; DB 6; Length 407;
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Best Local Similarity 98.5%; Pred. No. 8.5e-156;
Matches 391; Conservative 2; Mismatches 0; Indels 4; Gaps 2;

QY 18 RPLSSLSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGL 77
Db 1 RPLSSLSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGL 60

QY 78 YWTLNGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLP 137
Db 61 YWTLNGRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLP 119

QY 138 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLRYWYGDNTCEEYHTVGPHS 197
Db 120 PEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSKYLRYWYGDNTCEEYHTVGPHS 179

QY 198 CHIPKDALFTPYEIWEATNRLGSARSDVLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 257
Db 180 CHIPKDALFTPYEIWEATNRLGSARSDVLTLDVLDVVTTPPPDVHVSRRVGGLEDQLS 239

QY 258 VRWVSPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 317
Db 240 VRWVSPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSCLAGLKPGTVYFVQVRCN 299

QY 318 PFGIYGSKKAGIWSWSHPTAASRPRSGPGGVCPRGSGPVRRELKQFLGWL 377
Db 300 PFGIYGSKKAGIWSWSHPTAASRPRSGPGGVCPRGSGPVRRELKQFLGWL 359

QY 378 KKHAYCSNLSFRLYDQWRAMQSHKTRNQ---VLPA 411
Db 360 KKHAYCSNLSFRLYDQWRAMQSHKTRNQDEGILPS 396

RESULT 8
US-09-736-842-2
; Sequence 2, Application US/09736842
; Publication No. US20030228653A1
; GENERAL INFORMATION:
; APPLICANT: Masiaowski, Piotr
; TITLE OF INVENTION: No. US20030228653A1e1 Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/736,842
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US/09/120,601
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-736-842-2

Query Match          94.1%; Score 2118.5; DB 3; Length 405;
Best Local Similarity 98.7%; Pred. No. 9.2e-156;
Matches 389; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 21 SSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGLYWT 80
Db 1 SSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGLYWT 60

QY 81 LNGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLPPEK 140
Db 61 LNGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSTILAGSCLYVGLPPEK 120

QY 141 PFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLRYWYGDNTCEEYHTVGPHSCHI 200
Db 121 PFNISCWSRNKDLTCRWTPGAHGETFLHTNYSKYLRYWYGDNTCEEYHTVGPHSCHI 180

QY 201 PKDALFTPYEIWEATNRLGSARSDVLTLDVLDVVTTPPPDVHVSRRVGGLEDQLSVRW 260
Db 181 PKDALFTPYEIWEATNRLGSARSDVLTLDVLDVVTTPPPDVHVSRRVGGLEDQLSVRW 240
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QY 261 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQYVYFVQVRCNPF 320
DB 241 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQYVYFVQVRCNPF 300
QY 321 IYGSKAGIWSWSHPTASTPRSRPGRGGVCEPRGSGPVRRELKQFLGWLKX 380
DB 301 IYGSKAGIWSWSHPTASTPRSRPGRGGVCEPRGSGPVRRELKQFLGWLKX 360
QY 381 AYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411
DB 361 AYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 394

RESULT 9

US-10-074-901-2
; Sequence 2, Application US/10074901
; Publication No. US20020164785A1
; GENERAL INFORMATION:
; APPLICANT: Maslakowski, Piotr
; TITLE OF INVENTION: No. US20020164785A1 Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/10/074,901
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/012,072
; PRIOR FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-10-074-901-2

Query Match 94.1%; Score 2118.5; DB 4; Length 405;
Best Local Similarity 98.7%; Pred. No. 9.2e-156; Mismatches 0; Indels 3; Gaps 1;

Matches 389; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
QY 21 SLSWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQATCSIHGDTPGATAGLYWT 80
DB 1 SLSWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQATCSIHGDTPGATAGLYWT 60
QY 81 LNRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 140
DB 61 LNRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEK 120
QY 141 PNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNATCEYHTVGPSCHI 200
DB 121 PNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNATCEYHTVGPSCHI 180
QY 201 PKDLALFTPYEIWEATNRLGARSADVLTLDLVDVVTDPDPPDHVSRVGGLEDQLSVRW 260
DB 181 PKDLALFTPYEIWEATNRLGARSADVLTLDLVDVVTDPDPPDHVSRVGGLEDQLSVRW 240
QY 261 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQYVYFVQVRCNPF 320
DB 241 VSPALKDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLRLAGLKPQYVYFVQVRCNPF 300
QY 321 IYGSKAGIWSWSHPTASTPRSRPGRGGVCEPRGSGPVRRELKQFLGWLKX 380
DB 301 IYGSKAGIWSWSHPTASTPRSRPGRGGVCEPRGSGPVRRELKQFLGWLKX 360
QY 381 AYCSNLSFRLYDQWRAWMQSHKTRNQ---VLPA 411
DB 361 AYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPS 394

RESULT 10

US-10-247-463-4
; Sequence 4, Application US/10247463
; Publication No. US20030082734A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.

; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: DX09920
; CURRENT APPLICATION NUMBER: US/10/247,463
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 410
; TYPE: PRT
; ORGANISM: primate
US-10-247-463-4

Query Match 93.9%; Score 2114.5; DB 4; Length 410;
Best Local Similarity 94.7%; Pred. No. 1.9e-155;
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRPGVQAQARRPPRLSLSWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQ 60
DB 1 MPAGRPGVQAQARRPPRLSLSWSPLLLCVLGVRPGSGAHTAVISPODPTLLIGSSIQ 57
QY 61 ATCSIHGDTPGATAGLYWTNLRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSIHGDTPGATAGLYWTNLRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177
QY 181 YQDNATCEYHTVGPSCHI PKDLALFTPYEIWEATNRLGARSADVLTLDLVDVVTDP 240
DB 178 YQDNATCEYHTVGPSCHI PKDLALFTPYEIWEATNRLGARSADVLTLDLVDVVTDP 237
QY 241 PPDVHVS RVGGLEDQLSVRWSPAL KDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300
DB 238 PPDVHVS RVGGLEDQLSVRWSPAL KDPLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 297
QY 301 LAGLKPQYVYFVQVRCNPFYIGSKAGIWSWSHPTASTPRSRPGRGGVCEPRGSG 360
DB 298 LAGLKPQYVYFVQVRCNPFYIGSKAGIWSWSHPTASTPRSRPGRGGVCEPRGSG 357
QY 361 PSSGVRRELKQFLGWLKXAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAK 413
DB 358 PSSGVRRELKQFLGWLKXAYCSNLSFRLYDQWRAWMQSHKTRNQVLPAK 410

RESULT 11

US-10-778-002-12
; Sequence 12, Application US/10778002
; Publication No. US20040192891A1
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/10/778,002
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/521,335
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 410
; TYPE: PRT
; ORGANISM: primate

US-10-778-002-12

Query Match 93.9%; Score 2114.5; DB 4; Length 410;
Best Local Similarity 94.7%; Pred. No. 1.9e-155;
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRGPVQAQARRPPRLSSLSWPLLCVLGVRPGSGAHTAVISPODPTLLIGSSLLQ 60
DB 1 MPAGRRGPAQAQARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57

QY 61 ATCSIHGDTPGATAEGLYWTNGRLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDDPGATAEGLYWTNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 177

QY 181 YGQDNTCEYHTVGHPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240
DB 178 YGQDNTCEYHTVGHPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 237

QY 241 PPDVHVSRYGGLDQLSVRWSPPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSR 300
DB 238 PPDVHVSRYGGLDQLSVRWSPPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSR 297

QY 301 LAGLKPGTVYFVQVRCNPFYIYSGSKAGIWESEHPTAASPRSRPGRGGVCEPRGGE 360
DB 298 LAGLKPGTVYFVQVRCNPFYIYSGSKAGIWESEHPTAASPRSRPGRGGVCEPRGGE 357

QY 361 PSSGPRRELKQFLGWLKXHCYCSNLSFRLYDQWRAWMQSHKTRNOVLPK 413
DB 358 PSSGPRRELKQFLGWLKXHCYCSNLSFRLYDQWRAWMQSHKTRNOVLPK 410

RESULT 12
US-10-777-789-12
; Sequence 12, Application US/10777789
; Publication No. US20050048625A1
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/10/777,789
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/521,335
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 410
; TYPE: PRT
; ORGANISM: primate
US-10-777-789-12

Query Match 93.9%; Score 2114.5; DB 5; Length 410;
Best Local Similarity 94.7%; Pred. No. 1.9e-155;
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRGPVQAQARRPPRLSSLSWPLLCVLGVRPGSGAHTAVISPODPTLLIGSSLLQ 60
DB 1 MPAGRRGPAQAQARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57

QY 61 ATCSIHGDTPGATAEGLYWTNGRLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDDPGATAEGLYWTNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 177

QY 181 YGQDNTCEYHTVGHPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240
DB 178 YGQDNTCEYHTVGHPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 237

QY 241 PPDVHVSRYGGLDQLSVRWSPPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSR 300
DB 238 PPDVHVSRYGGLDQLSVRWSPPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSR 297

QY 301 LAGLKPGTVYFVQVRCNPFYIYSGSKAGIWESEHPTAASPRSRPGRGGVCEPRGGE 360
DB 298 LAGLKPGTVYFVQVRCNPFYIYSGSKAGIWESEHPTAASPRSRPGRGGVCEPRGGE 357

QY 361 PSSGPRRELKQFLGWLKXHCYCSNLSFRLYDQWRAWMQSHKTRNOVLPK 413
DB 358 PSSGPRRELKQFLGWLKXHCYCSNLSFRLYDQWRAWMQSHKTRNOVLPK 410

RESULT 13
US-11-016-106-4
; Sequence 4, Application US/11016106
; Publication No. US20050106673A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; FILE REFERENCE: DX0992Q
; CURRENT APPLICATION NUMBER: US/11/016,106
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 410
; TYPE: PRT
; ORGANISM: primate
US-11-016-106-4

Query Match 93.9%; Score 2114.5; DB 6; Length 410;
Best Local Similarity 94.7%; Pred. No. 1.9e-155;
Matches 391; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRGPVQAQARRPPRLSSLSWPLLCVLGVRPGSGAHTAVISPODPTLLIGSSLLQ 60
DB 1 MPAGRRGPAQAQARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 57

QY 61 ATCSIHGDTPGATAEGLYWTNGRLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDDPGATAEGLYWTNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLYKLRW 177

QY 181 YGQDNTCEYHTVGHPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 240
DB 178 YGQDNTCEYHTVGHPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDVLDVTTDP 237

QY 241 PPDVHVSRYGGLDQLSVRWSPPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSR 300
DB 238 PPDVHVSRYGGLDQLSVRWSPPALKDFLFOAKYQIRYRVSDVDWKVDDVSNQTSR 297

QY 301 LAGLKPGTVYFVQVRCNPFYIYSGSKAGIWESEHPTAASPRSRPGRGGVCEPRGGE 360
DB 298 LAGLKPGTVYFVQVRCNPFYIYSGSKAGIWESEHPTAASPRSRPGRGGVCEPRGGE 357

QY 361 PSSGPRRELKQFLGWLKXHCYCSNLSFRLYDQWRAWMQSHKTRNOVLPK 413
DB 358 PSSGPRRELKQFLGWLKXHCYCSNLSFRLYDQWRAWMQSHKTRNOVLPK 410

Db 358 PSSGPFVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVLPDKL 410

RESULT 14
US-09-880-578-4
; Sequence 4, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmsberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-880-578-4

Query Match 93.2%; Score 2098; DB 3; Length 425;
Best Local Similarity 91.1%; Pred. No. 3.8e-154;
Matches 391; Conservative 5; Mismatches 13; Indels 20; Gaps 3;
QY 1 MPAGRPGVQAQSARRPPRLSSLSWSPLLLCVLGVPGRGSGAHTAVTISPODPTLLIGSSSLQ 60
Db 1 MPAGRRGPAQAQSARRPP-PLLP-LLLCVLGAPRAGSGAHTAVTISPODPTLLIGSSSL 56
QY 61 ATCSIHGDTPGATAGLYTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
Db 57 ATCSVHGDPFGATAGLYTLNGRLPSELRLNASTLALANLNGSRQSGDNLVCH 116
QY 121 ARDGSILAGSCLVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
Db 117 ARDGSILAGSCLVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 176
QY 181 YQDNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTTDP 240

Db 177 YQDNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTTDP 236
QY 241 PPDVHVSRYGGLDQLSVRWVSPPALKDFLQAKQIRYRVDSVDWKVVDVSNQTSR 300
Db 237 PPDVHVSRYGGLDQLSVRWVSPPALKDFLQAKQIRYRVDSVDWKVVDVSNQTSR 296
QY 301 LAGLKPGTVYFQVRCNPFYIYSGKKAGIWSWSHPTAASTPRSERPGPGGGVCEPRGGE 360
Db 297 LAGLKPGTVYFQVRCNPFYIYSGKKAGIWSWSHPTAASTPRSERPGPGGGVCEPRGGE 356
QY 361 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----- 407
Db 357 PSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQSGCPRADGA 416
QY 408 ---VLPKAL 413
Db 417 RREVLPDKL 425

RESULT 15
US-09-037-657-44
; Sequence 44, Application US/09037657A
; Patent No. US20020045741A1
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; APPLICANT: Nicola, Nicos A.
; APPLICANT: Farley, Alison
; APPLICANT: Wilson, Tracy
; APPLICANT: Zhang, Jian-Guo
; APPLICANT: Alexander, Warren
; APPLICANT: Rakar, Steven
; APPLICANT: Fabri, Louis
; APPLICANT: Koima, Tetsuo
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Kikuchi, Yasufumi
; APPLICANT: Nash, Andrew
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
; FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
; CURRENT APPLICATION NUMBER: US/09/037,657A
; CURRENT FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 08/928,720
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Amino Acid Sequence of NR6
US-09-037-657-44

Query Match 93.2%; Score 2097.5; DB 3; Length 421;
Best Local Similarity 93.7%; Pred. No. 4.1e-154;
Matches 388; Conservative 7; Mismatches 12; Indels 7; Gaps 3;
QY 1 MPAGRPGVQAQSARRPPRLSSLSWSPLLLCVLGVPGRGSGAHTAVTISPODPTLLIGSSSLQ 60
Db 1 MPAGRRGPAQAQSARRPP-PLLP-LLLCVLGAPRAGSGAHTAVTISPODPTLLIGSSSL 56
QY 61 ATCSIHGDTPGATAGLYTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
Db 57 ATCSVHGDPFGATAGLYTLNGRLPSELRLNASTLALANLNGSRQSGDNLVCH 116
QY 121 ARDGSILAGSCLVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
Db 117 ARDGSILAGSCLVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYLKRW 176
QY 181 YQDNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTTDP 240
Db 177 YQDNTCEBYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTTDP 236

Qy	241	PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR	300
Db	237	PPDVHVSRYGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCR	296
Qy	301	LAGLXPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGGE	360
Db	297	LAGLXPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGGGVCEPRGGE	356
Qy	361	PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---	411
Db	357	PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPS	410

Search completed: April 11, 2006, 02:43:00
Job time : 97.1152 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:03:38 ; Search time 116.124 Seconds
(without alignments)
1608.075 Million cell updates/sec

Title: US-09-037-657-15

Perfect score: 2317

Sequence: 1 MPAGRPGPVAQSRAPRPL.....NODEGILPGRGAARGPAG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2317	100.0	425	2 AAW55012	Novel hae
2	2317	100.0	425	3 AAY93659	PA Aay93659 A murine
3	2317	100.0	425	4 AAE00821	PA Aae00821 Murine ha
4	2313	99.8	425	2 AAW59804	Aaw59804 Nucleotid
5	2313	99.8	425	2 AAY26337	Aay26337 Murine U4
6	2288	98.7	425	2 AAW70862	Aaw70862 Rat Zcyto
7	2226.5	96.1	413	2 AAW55011	Novel hae
8	2226.5	96.1	413	3 AAY93658	Aay93658 A murine
9	2226.5	96.1	413	4 AAE00820	Murine ha
10	2225	96.0	416	2 AAY29780	Mouse DNA
11	2209.5	95.4	407	3 AAB19589	Aabi9589 Mouse cyt
12	2209.5	95.4	407	4 AAB36648	Mouse cyt
13	2209.5	95.4	407	7 ADC07180	Mouse cyt
14	2209.5	95.4	407	8 ADT90845	Mouse cyt
15	2209.5	95.4	407	8 ADT61033	Mouse cyt
16	2209.5	95.4	407	8 ADY57158	Mouse cyt
17	2209.5	95.4	407	9 ADZ65015	Mouse NR6
18	2209	95.3	405	2 AAY15214	Aay15214 Amino aci
19	2209	95.3	405	3 AAY44839	Mouse orp
20	2178	94.0	421	4 AAE00826	Murine ha
21	2176.5	93.9	422	2 AAY05782	Human typ
22	2176.5	93.9	422	2 AAY06479	Human typ
23	2176.5	93.9	422	2 AAY17825	Human PRO
24	2176.5	93.9	422	2 AAY26339	Human U4

RESULT 1

AAW55012

ID AAW55012 standard; protein; 425 AA.

XX AC AAW55012;

XX DT 29-SEP-1998 (first entry)

XX DE Novel haemopoietin receptor NR6.2 protein.

XX KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;

XX KW cell survival; therapeutic; neuronal proliferation; drug screening;

XX KW Mouse.

XX OS Mus sp.

XX PN WO9811225-A2.

XX PD 19-MAR-1998.

XX PF 11-SEP-1997; 97WO-GB002479.

XX PR 11-SEP-1996; 96AU-00002246.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX (DZIE/) DZIEGLEWSKA H E.

XX Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;

XX Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;

XX WPI: 1998-260970/23.

XX DR N-PSDB; AAV27141.

XX PT New isolated haemopoietin receptor - used for developing products for

XX modulating proliferation, differentiation and survival of cells, e.g.

XX neuronal cells.

XX Claim 15; Page 84-87; 182pp; English.

XX The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6.

XX Interaction between the novel HR and a ligand facilitates proliferation,

XX differentiation and survival of a wide variety of cells. The HR and it's

XX derivatives can be used for modulating the activity of the receptors e.g.

XX to regulate development, maintenance or regeneration in an array of

XX different cells and tissues in vitro and in vivo. They can be present in

XX therapeutics used for modulating neuronal proliferation, differentiation

XX and survival. The products can also be used for detection and diagnosis,

XX

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CC e.g. for cancers or predisposition to cancers, or for drug screening
 XX
 SQ Sequence 425 AA;

Query Match 100.0%; Score 2317; DB 2; Length 425;
 Best Local Similarity 100.0%; Pred. No. 8e-193;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRPGVVAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLIQ 60
 DB 1 MPAGRPGVVAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLIQ 60

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEYHTVGPVHSCHPKDLALFTPEIWEATNRLGARSDDLTLVDLVVTTDP 240
 DB 181 YQDNTCEYHTVGPVHSCHPKDLALFTPEIWEATNRLGARSDDLTLVDLVVTTDP 240

QY 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300
 DB 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300

QY 301 LAGLKPCTVYFVQVRCNPFYIYGSKAGIWSWSHPTAASPRSERPGGGVCEPRGGE 360
 DB 301 LAGLKPCTVYFVQVRCNPFYIYGSKAGIWSWSHPTAASPRSERPGGGVCEPRGGE 360

QY 361 PSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIILPSGRGAA 420
 DB 361 PSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIILPSGRGAA 420

QY 421 RGPAG 425
 DB 421 RGPAG 425

RESULT 2
 AAY93659
 ID AAY93659 standard; protein; 425 AA.
 AC AAY93659;
 XX
 XX 25-SEP-2000 (first entry)
 DT
 DE A murine hemopoietin receptor NR6.2 polypeptide.
 XX
 XX Haemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation;
 KW hemopoietic progenitor cell; cancer; apoptosis; postnatal survival;
 KW suckling; postnatal baby; foetal testing.
 XX
 OS Mus musculus.
 XX
 PN WO200035471-A1.
 XX
 PD 22-JUN-2000.
 XX
 XX 17-DEC-1999; 99WO-AU001119.
 XX
 XX 17-DEC-1998; 98AU-00007762.
 PR
 XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 XX
 XX Alexander WS, Metcalf D;
 PI
 XX WFI; 2000-442273/38.
 XX
 DR N-PSDB; AAA46792.
 XX
 PT Administering the hemopoietin receptor NR6 is used to modulate production

PT of hemopoietic progenitor cells and facilitate postnatal survival of
 PT mammals by inducing or promoting suckling.
 XX
 PS Claim 5; Page 73-74; 77pp; English.
 XX
 CC The present sequence represents a murine haemopoietin receptor NR6 (CLF-
 CC 1) polypeptide. The specification describes a method for the treatment or
 CC prophylaxis of disease conditions associated with dysfunctional
 CC haemopoietic regulation. The method comprises modulating the production
 CC of hemopoietic progenitor cells in a mammal by administering the NR6.
 CC Decreasing production of progenitor cells may be used in the treatment of
 CC cancer or to induce apoptosis of particular cell types. Increasing
 CC production of progenitor cells is used to facilitate postnatal survival
 CC in mammals by inducing or promoting suckling. Potential disease
 CC conditions may be identified by monitoring NR6 production in postnatal
 CC babies or allowing expectant mothers to undergo foetal testing. Low NR6
 CC levels can then be treated immediately
 XX
 SQ Sequence 425 AA;

Query Match 100.0%; Score 2317; DB 3; Length 425;
 Best Local Similarity 100.0%; Pred. No. 8e-193;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRPGVVAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLIQ 60
 DB 1 MPAGRPGVVAQSARRPRPLSLWSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLIQ 60

QY 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGATAGLYWTLNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEYHTVGPVHSCHPKDLALFTPEIWEATNRLGARSDDLTLVDLVVTTDP 240
 DB 181 YQDNTCEYHTVGPVHSCHPKDLALFTPEIWEATNRLGARSDDLTLVDLVVTTDP 240

QY 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300
 DB 241 PPDVHVSVRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300

QY 301 LAGLKPCTVYFVQVRCNPFYIYGSKAGIWSWSHPTAASPRSERPGGGVCEPRGGE 360
 DB 301 LAGLKPCTVYFVQVRCNPFYIYGSKAGIWSWSHPTAASPRSERPGGGVCEPRGGE 360

QY 361 PSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIILPSGRGAA 420
 DB 361 PSSGPVRRLEKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIILPSGRGAA 420

QY 421 RGPAG 425
 DB 421 RGPAG 425

RESULT 3
 AAE00821
 ID AAE00821 standard; protein; 425 AA.
 XX
 AC AAE00821;
 XX
 XX 09-SEP-2004 (revised)
 DT 02-JUL-2001 (first entry)
 XX
 XX Murine haemopoietin receptor, NR6.2 isoform.
 DE
 XX Murine; biologically active complex; haemopoietin receptor; NR6;
 KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
 KW differentiation; cell survival; neurotrophic activity.
 XX
 OS Mus sp.

OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Domain 330..334
 XX /label = WSXWS_motif
 XX WO200127157-A1.
 XX 19-APR-2001.
 XX 06-OCT-2000; 2000WO-AU001216.
 XX 08-OCT-1999; 99AU-00003327.
 PR 12-MAY-2000; 2000AU-00007489.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX PA Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
 PI Nakata Y, Hasegawa M;
 XX WPI; 2001-281978/29.
 DR N-PSDB; AAD04193.
 XX New biologically active complex comprising NR6 and cardiostrophin-like-
 PT cytokine, for facilitating proliferation, differentiation and/or survival
 PT of a cell.
 XX Claim 26; Page 81-83; 123pp; English.
 XX The present invention relates to a biologically active complex comprising
 CC a haemopoietin receptor, NR6 and cardiostrophin-like cytokine (CLC). The
 CC complex is useful in the manufacture of a medicament for the treatment
 CC and/or prophylaxis of a subject, as it is involved in facilitating
 CC proliferation, differentiation and/or survival of a cell. The complex or
 CC its components have neurotrophic activity. The present sequence is murine
 CC haemopoietin receptor, NR6.2 isoform. The NR6.2 represents the NR6 splice
 CC variant obtained due to alternative mRNA splicing
 CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
 XX Sequence 425 AA;
 SQ
 Query Match 100.0%; Score 2317; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 8e-193;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAGRPGVQAQARRPPRLSLSWSPLLLCVLGVRGSGAHTAVISQDPPTLLIGSSLIQ 60
 DB 1 MPAGRPGVQAQARRPPRLSLSWSPLLLCVLGVRGSGAHTAVISQDPPTLLIGSSLIQ 60
 QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLYVGLPPEKPFNISCWNRNMDLTCRWTGAGHGETFLHTNYSKYKLRW 180
 DB 121 ARDGSILAGSCLYVGLPPEKPFNISCWNRNMDLTCRWTGAGHGETFLHTNYSKYKLRW 180
 QY 181 YQDNTCEYHTVGPVPHSCHIPKDALFPTPEIWEATNRLGSRSDVLTLDVLDVVTTPD 240
 DB 181 YQDNTCEYHTVGPVPHSCHIPKDALFPTPEIWEATNRLGSRSDVLTLDVLDVVTTPD 240
 QY 241 PPDVHVSVRGGLDQSLVSRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300
 DB 241 PPDVHVSVRGGLDQSLVSRWSPPALKDFLFOAKYQIRYVEDSVDMKVVDDVSNQTSR 300
 QY 301 LAGLKGTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSERPGGVCPRGGE 360
 DB 301 LAGLKGTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSERPGGVCPRGGE 360
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNDEGILPSRRGAA 420
 DB 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNDEGILPSRRGAA 420

QY 421 RGPAG 425
 DB 421 RGPAG 425
 RESULT 4
 AAW59804
 ID AAW59804 standard; protein; 425 AA.
 XX AC AAW59804;
 XX 26-OCT-1998 (first entry)
 XX Nucleotide sequence of the murine U4 protein.
 XX Murine; U4 protein; haematopoietin receptor superfamily;
 KW cell proliferation; immune response; antibody; cell differentiation;
 KW autoimmune disease; cancer; allergy.
 XX Mus sp.
 XX WO9831811-A1.
 XX 23-JUL-1998.
 XX 15-JAN-1998; 98WO-US000334.
 XX 16-JAN-1997; 97US-00784863.
 XX (GENY) GENETICS INST INC.
 XX Donaldson DD, Collins M, Neben T, Whitters M;
 DR WPI; 1998-414109/35.
 DR N-PSDB; AAV41688.
 XX New nucleic acid encoding U4 haematopoietin receptor superfamily chain -
 PT potentially useful, e.g. for modulating cell proliferation or immune
 PT response, for treating cancer and auto-immune disease.
 XX Claim 9; Page 26-27; 38pp; English.
 XX This is the amino acid sequence of the murine U4 protein from the
 CC haematopoietin receptor superfamily, used in the method of the invention
 CC for the modulation of cell proliferation, or the immune response.
 CC Transformed mammalian cells are used to produce recombinant U4 protein.
 CC The U4 protein is used to screen for specific binding agents, raise
 CC antibodies. It is also used as reagents for assays and as tissue markers
 CC for isolation of cognate ligands and receptors, and in pharmaceutical
 CC compositions which may modulate cell proliferation, cell differentiation,
 CC and the immune system (e.g. for treating immune deficiency, inherited or
 CC the result of infection, autoimmune diseases, cancer, and allergy)
 XX Sequence 425 AA;
 Query Match 99.8%; Score 2313; DB 2; Length 425;
 Best Local Similarity 99.8%; Pred. No. 1.8e-192;
 Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPAGRPGVQAQARRPPRLSLSWSPLLLCVLGVRGSGAHTAVISQDPPTLLIGSSLIQ 60
 DB 1 MPAGRPGVQAQARRPPRLSLSWSPLLLCVLGVRGSGAHTAVISQDPPTLLIGSSLIQ 60
 QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLYVGLPPEKPFNISCWNRNMDLTCRWTGAGHGETFLHTNYSKYKLRW 180
 DB 121 ARDGSILAGSCLYVGLPPEKPFNISCWNRNMDLTCRWTGAGHGETFLHTNYSKYKLRW 180
 QY 181 YQDNTCEYHTVGPVPHSCHIPKDALFPTPEIWEATNRLGSRSDVLTLDVLDVVTTPD 240

Db 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDVLTLDVLDVVTDP 240
Qy 241 PPDVHVSRVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300
Db 241 PPDVHVSRVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300
Qy 301 LAGLKPGTVYFVQVRCNPFGIYVSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360
Db 301 LAGLKPGTVYFVQVRCNPFGIYVSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360
Qy 361 PSSGPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSGRGAA 420
Db 361 PSSGPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSGRGAA 420
Qy 421 RGPAG 425
Db 421 RGPAG 425
RESULT 5
AAW26337
ID AAW26337 standard; protein; 425 AA.
XX AC AAY26337;
XX DT 13-JAN-2000 (first entry)
XX DE Murine U4 haematopoietin receptor superfamily chain.
XX KW Murine U4 protein; haematopoietin receptor superfamily;
KW biological activity; cytokine; cell proliferation; cell differentiation;
KW immune stimulation; immune suppression; haematopoiesis regulation;
KW immune disorder; immune deficiency; autoimmune disorder; allergy; cancer;
KW myeloid cell; lymphoid cell deficiency; platelet disorder.
XX OS Mus sp.
XX FH Location/Qualifiers
FT Peptide 1: 40
FT /label= Putative_signal_sequence
FT Protein 41..383
FT /label= Mature_murine_U4
XX WO9953066-A1.
XX PD 21-OCT-1999.
XX PF 09-APR-1999; 99WO-US007882.
XX PR 10-APR-1998; 98US-00058660.
XX PA (GEM) GENETICS INST INC.
XX PI Donaldson D, Collins M, Whitters M, Neben T;
XX WPI; 1999-611303/52.
XX N-PSDB; AAX90752.
XX Novel polypeptides and polynucleotides used for treatment of human
PT diseases and disorders e.g. immune disorders or deficiencies caused by
PT fungal, parasitic or viral infections.
XX Claim 9; Page 31-32; 43pp; English.
XX The present sequence is a murine U4 protein which is a member of
CC haematopoietin receptor superfamily. The protein sequence has conserved
CC cysteine pairs and WSXWS motifs characteristic of the receptor family. It
CC is predicted to have the following biological activities: cytokine, cell
CC proliferation/differentiation, immune stimulating or suppressing and
CC haematopoiesis regulating. The U4 protein can be used to treat immune
CC disorders and deficiencies, autoimmune disorders, allergies, cancer,
CC myeloid or lymphoid cell deficiencies and platelet disorders

XX SQ Sequence 425 AA;
Query Match 99.8%; Score 2313; DB 2; Length 425;
Best Local Similarity 99.8%; Pred. No. 1.8e-192;
Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MPAGRPGVAQSARRPPRLSSLSWPLLLCVLGPVPGSGAHTAVISPODPTLLIGSSIQ 60
Db 1 MPAGRPGVAQSARRPPRLSSLSWPLLLCVLGPVPGSGAHTAVISPODPTLLIGSSIQ 60
Qy 61 ATCSIHGDTPTGATAGELVWTLNGRRLPSELRLNTSTLALANLNGSRQOSGDNLVCH 120
Db 61 ATCSIHGDTPTGATAGELVWTLNGRRLPSELRLNTSTLALANLNGSRQOSGDNLVCH 120
Qy 121 ARDGSILAGSCLYVGLPPEKPFNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
Db 121 ARDGSILAGSCLYVGLPPEKPFNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
Qy 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDVLTLDVLDVVTDP 240
Db 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDVLTLDVLDVVTDP 240
Qy 241 PPDVHVSRVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300
Db 241 PPDVHVSRVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSR 300
Qy 301 LAGLKPGTVYFVQVRCNPFGIYVSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360
Db 301 LAGLKPGTVYFVQVRCNPFGIYVSKAGIWSWSHPTAASPRSRPFGGVCBPRGGE 360
Qy 361 PSSGPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSGRGAA 420
Db 361 PSSGPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQGILPSGRGAA 420
Qy 421 RGPAG 425
Db 421 RGPAG 425
RESULT 6
AAW70862
ID AAW70862 standard; protein; 425 AA.
XX AC AAW70862;
XX DT 17-MAR-1999 (first entry)
XX DE Rat Zcytor5 protein.
XX KW Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; Zcytor5 ligand.
XX OS Rattus sp.
XX WO9849307-A1.
XX PD 05-NOV-1998.
XX PF 01-MAY-1998; 98WO-US008865.
XX PR 01-MAY-1997; 97US-0045287P.
XX PR 01-MAY-1997; 97US-00850030.
XX PR 13-FEB-1998; 98US-00023890.
XX PR 13-FEB-1998; 98US-0074721P.
XX (ZYMO) ZYMOGENETICS INC.
XX PA Lok S, Prensell SR, Jelmeberg AC, Gilbert T, Whitmore TB;
XX PI Foster DC, Adams RL, Lehner JW;
XX WPI; 1999-034662/03.
DR

DR N-PSDB; AAV70896.
 XX
 PT New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-
 PT regulating Zcytor5 natural ligands or detecting cardiotrophin-1 in blood.
 XX
 PS Claim 1; Page 75-76; 55pp; English.
 XX

CC The present sequence represents a protein designated Zcytor5, which is a
 CC cytokinin-like receptor. Soluble Zcytors may be administered to down-
 CC regulate the effects of a growth and/or maintenance factor in thyroid,
 CC heart, and skeletal muscle for example to lessen the effect of
 CC cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement.
 CC Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to
 CC discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA
 CC or RNA can be used to determine the presence and integrity of the Zcytor5
 CC gene on chromosome 19. Antibodies and the anti-idiotypic antibody could
 CC be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand
 CC effects
 XX

XX Sequence 425 AA;

Query Match 98.7%; Score 2288; DB 2; Length 425;
 Best Local Similarity 98.8%; Pred. No. 2.7e-190; Indels 0; Gaps 0;
 Matches 420; Conservative 1; Mismatches 4;
 QY 1 MPAGRPGVQAQSARPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSIQ 60
 DB 1 MPAGRPGVQAQSARPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSIH 60
 QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240
 DB 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240
 QY 241 PPDVHVSVRVGLLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSCR 300
 DB 241 PPDVHVSVRVGLLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSCR 300
 QY 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360
 DB 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIPLPSGRGAA 420
 DB 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIPLPSGRGAA 420
 QY 421 RGPAG 425
 DB 421 RGPAG 425

RESULT 7

AAW5011
 ID AAW5011 standard; protein; 413 AA.

XX AAW5011;

XX 29-SEP-1998 (first entry)

DE Novel haemopoietin receptor NR6.1 protein.

KW Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
 KW cell survival; therapeutic; neuronal proliferation; drug screening;
 KW Mouse.

OS Mus sp.

XX WO9811225-A2.
 XX
 PD 19-MAR-1998.
 XX

XX 11-SEP-1997; 97WO-GB002479.
 XX

XX 11-SEP-1996; 96AU-00002246.
 XX (AMRA-) AMRAD OPERATIONS PTY LTD.
 XX (DZIE/) DZIEGLEWSKA H E.

XX Hilton DJ, Nicola NA, Farley A, Willson T, Zhang J, Alexander W;
 XX Rakar S, Fabri L, Kojima T, Maeda M, Kikuchi Y, Nash A;
 XX WPI: 1998-260970/23.
 XX N-PSDB; AAV27140.
 XX

XX New isolated haemopoietin receptor - used for developing products for
 PT modulating proliferation, differentiation and survival of cells, e.g.
 PT neuronal cells.
 XX

XX Claim 14; Page 77-81; 182pp; English.

XX The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6.
 CC Interaction between the novel HR and a ligand facilitates proliferation,
 CC differentiation and survival of a wide variety of cells. The HR and it's
 CC derivatives can be used for modulating the activity of the receptors e.g.
 CC to regulate development, maintenance or regeneration in an array of
 CC different cells and tissues in vitro and in vivo. They can be present in
 CC therapeutics used for modulating neuronal proliferation, differentiation
 CC and survival. The products can also be used for detection and diagnosis,
 CC e.g. for cancers or predisposition to cancers, or for drug screening
 XX

XX Sequence 413 AA;

Query Match 96.1%; Score 2226.5; DB 2; Length 413;
 Best Local Similarity 98.8%; Pred. No. 5.9e-185;
 Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRPGVQAQSARPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSIQ 60
 DB 1 MPAGRPGVQAQSARPPRLSLWSPLLLCVLGVPRGSGAHTAVISPODPTLLIGSSIQ 60
 QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 DB 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
 QY 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240
 DB 181 YQDNTCEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSDDLTLVDLVVTTDP 240
 QY 241 PPDVHVSVRVGLLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSCR 300
 DB 241 PPDVHVSVRVGLLEDQLSVRWVSPALKDPLFOAKYQIRYRVSDSDVMDVDSNQTSCR 300
 QY 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360
 DB 301 LAGLKPVTYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRSRPFGGVCPRGGE 360
 QY 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIPLPS 414
 DB 361 PSSGPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDGIPLPS 414

RESULT 8

AAW93658
 ID AAW93658 standard; protein; 413 AA.

XX

AC AAY93658;
XX 25-SEP-2000 (first entry)
XX A murine haemopoietin receptor NR6.1 polypeptide.
DE Haemopoietin receptor NR6; CLF-1; dysfunctional haemopoietic regulation;
KW hemopoietic progenitor cell; cancer; apoptosis; postnatal survival;
KW suckling; postnatal baby; foetal testing.
XX Mus musculus.
XX WO200035471-A1.
XX 22-JUN-2000.
XX 17-DEC-1999; 99WO-AU001119.
XX 17-DEC-1998; 98AU-00007762.
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX Alexander WS, Metcalf D;
XX WPI; 2000-442273/38.
XX N-PSDB; AAA46791.
XX Administering the hemopoietin receptor NR6 is used to modulate production
XX of hemopoietic progenitor cells and facilitate postnatal survival of
XX mammals by inducing or promoting suckling.
XX Claim 5; Page 70-71; 77pp; English.
XX The present sequence represents a murine haemopoietin receptor NR6 (CLF-
XX 1) polypeptide. The specification describes a method for the treatment or
XX prophylaxis of disease conditions associated with dysfunctional
XX haemopoietic regulation. The method comprises modulating the production
XX of hemopoietic progenitor cells in a mammal by administration of NR6.
XX Decreasing production of progenitor cells may be used in the treatment of
XX cancer or to induce apoptosis of particular cell types. Increasing
XX production of progenitor cells is used to facilitate postnatal survival
XX in mammals by inducing or promoting suckling. Potential disease
XX conditions may be identified by monitoring NR6 production in postnatal
XX babies or allowing expectant mothers to undergo foetal testing. Low NR6
XX levels can then be treated immediately
XX Sequence 413 AA;
Query Match 96.1%; Score 2226.5; DB 3; Length 413;
Best Local Similarity 98.8%; Pred. No. 5.9e-185;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
QY 1 MPAGRGPVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLQ 60
DB 1 MPAGRGPVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLQ 60
QY 61 ATCSIHGDTPGAETAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 61 ATCSIHGDTPGAETAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYLKW 180
DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSKYLKW 180
QY 181 YGQDNCTCEEVHTVGRHSCHIPKDALFTPEIWEATNRLGARSVDLTDVLDVTTDP 240
DB 181 YGQDNCTCEEVHTVGRHSCHIPKDALFTPEIWEATNRLGARSVDLTDVLDVTTDP 240
QY 241 PPDVHVSVRGLEDQLSVRWVSPALKDQFLQAKYQIRYRVEDSVWKVVDVDSNQTSCR 300
DB 241 PPDVHVSVRGLEDQLSVRWVSPALKDQFLQAKYQIRYRVEDSVWKVVDVDSNQTSCR 300
QY 301 LAGLKPQTVYFVQRCNPFGIYGSKKAGIWSWSHPTAASPRSRPFGGVCERPGGE 360

DB 301 LAGLKPQTVYFVQRCNPFGIYGSKKAGIWSWSHPTAASPRSRPFGGVCERPGGE 360
QY 361 PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQSKHTRNQDGIPLS 414
DB 361 PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQSKHTRNQ---VLPA 411
RESULT 9
AAE00820
ID AAE00820 standard; protein; 413 AA.
XX AAE00820;
XX 09-SEP-2004 (revised)
DT 02-JUL-2001 (first entry)
XX Murine haemopoietin receptor, NR6.1 isoform.
XX Murine; biologically active complex; haemopoietin receptor; NR6;
KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
KW differentiation; cell survival; neurotrophic activity.
XX Mus sp.
OS Unidentified.
XX Key Location/Qualifiers
FH Domain 330..334
FT /label = WSXWS_motif
XX WO200127157-A1.
XX 19-APR-2001.
XX 06-OCT-2000; 2000WO-AU001216.
XX 08-OCT-1999; 99AU-00003327.
PR 12-MAY-2000; 2000AU-00007489.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
PI Nakata Y, Hasegawa M;
XX WPI; 2001-281978/29.
DR N-PSDB; AAD04192.
XX New biologically active complex comprising NR6 and cardiotrophin-like-
PT cytokine, for facilitating proliferation, differentiation and/or survival
PT of a cell.
XX Claim 25; Page 76-77; 123pp; English.
XX The present invention relates to a biologically active complex comprising
CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC). The
CC complex is useful in the manufacture of a medicament for the treatment
CC and/or prophylaxis of a subject, as it is involved in facilitating
CC proliferation, differentiation and/or survival of a cell. The complex or
CC its components have neurotrophic activity. The present sequence is murine
CC haemopoietin receptor, NR6.1 isoform. The NR6.1 represents the NR6 splice
CC variant obtained due to alternative mRNA splicing
CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX Sequence 413 AA;
Query Match 96.1%; Score 2226.5; DB 4; Length 413;
Best Local Similarity 98.8%; Pred. No. 5.9e-185;
Matches 409; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
QY 1 MPAGRGPVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLQ 60
DB 1 MPAGRGPVQAQARRPRPRLSSLSWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLQ 60

QY 61 ATCSIHGDTGATAEGLYWTNGRRPLSELSRLINTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTGATAEGLYWTNGRRPLSELSRLINTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKW 180
 DB 121 ARDGSILAGSCLVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKW 180
 QY 181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTDP 240
 DB 181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTDP 240
 QY 241 PPDVHSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSR 300
 DB 241 PPDVHSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSR 300
 QY 301 LAGLKPGTVVYFQVRCNPFPGIYSGKKAGIWESEHPTAASTPRSERPGGGVCEPRGGE 360
 DB 301 LAGLKPGTVVYFQVRCNPFPGIYSGKKAGIWESEHPTAASTPRSERPGGGVCEPRGGE 360
 QY 361 PSSGPPVRRRELKQFLGMLKKHAYCSNLSFRLYDQWRAMWQSKHTRNQDEGILPS 414
 DB 361 PSSGPPVRRRELKQFLGMLKKHAYCSNLSFRLYDQWRAMWQSKHTRNQ---VLPA 411

RESULT 10

AAV29780

ID AAV29780 standard; protein; 416 AA.

XX AC

AAV29780;

XX XX

DT 04-NOV-1999 (first entry)

XX DE

Mouse DNAX soluble receptor subunit 1.

XX KW

DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
 interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;
 inflammatory disorder; inflammatory response; innate immunity;
 morphogenic development; immunological disorder.

XX OS

Mus sp.

XX PN

WO9940195-A1.

XX PD

12-AUG-1999.

XX PF

05-FEB-1999; 99WO-US002600.

XX PR

06-FEB-1998; 98US-0073941P.

XX PR

13-MAY-1998; 98US-00078194.

XX PA

(SCHE) SCHERING CORP.

XX PI

Mattson JD, Mcclanahan TK, Kastelein RA;

XX DR

WPI; 1999-527306/44.

XX DR

N-PSDB; AA208862.

XX PT

New receptor subunits useful in the treatment inflammatory disorders.

XX PS

Claim 2; Page 24-25; 133pp; English.

XX CC

The present invention describes a composition (I) comprising DNAX
 cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
 subunit I (DSRS1) protein, which together encode a new mammalian cytokine
 -related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or
 DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRS1 is useful for
 screening for ligands (i.e. agonists/antagonists) from a library of
 compounds, which are useful for modulating the physiology or development
 of a cell or tissue culture e.g. inflammatory responses, innate immunity
 and/or morphogenic development. (R), antibodies and ligands are useful
 for treatment of conditions, especially immunological disorders,

CC associated with conditions exhibiting abnormal expression of (R). (R) is
 useful as a phosphate labeling enzyme to label substrates, and the
 CC subunits DSRs1 and DCRS1 are useful as immunogens for generating
 CC antibodies, or as antigens for binding antibodies. Nucleic acids encoding
 CC (R) are useful for identifying related DNAs and mRNAs, and variants from
 CC other individuals or species. The present sequence represents the
 CC specifically claimed mouse DSRs1, for use in the composition of the
 CC present invention

XX SQ Sequence 416 AA;

Query Match 96.0%; Score 2225; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8e-185;
 Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RPLSSLSWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGL 77
 DB 9 RPLSSLSWSPLLLCVLGVRGGGAHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGL 68

QY 78 YWTNGRRRLPSELSRLINTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLVYGLP 137
 DB 69 YWTNGRRRLPSELSRLINTSTLALANLNGSRQSGDNLVCHARDGSILAGSCLVYGLP 128

QY 138 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKWYQDNTCEEYHTVGPHS 197
 DB 129 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKWYQDNTCEEYHTVGPHS 188

QY 198 CHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTDPDPVHVSRVGLEDQLS 257
 DB 189 CHIPKDLALFTPYEIWVEATNRLGARSVDLTLDVLDVVTDPDPVHVSRVGLEDQLS 248

QY 258 VRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSCLAGLKPGTVVYFQVRCN 317
 DB 249 VRWVSPALKDFLFOAKYQIRYRVSDVWKVVDVSNQTSCLAGLKPGTVVYFQVRCN 308

QY 318 PFGIYSGKKAGIWESEHPTAASTPRSERPGGGVCEPRGSGPVRRELKQFLGWL 377
 DB 309 PFGIYSGKKAGIWESEHPTAASTPRSERPGGGVCEPRGSGPVRRELKQFLGWL 368

QY 378 KKHAYCSNLSFRLYDQWRAMWQSKHTRNQDEGILPSGRGAARGPAG 425
 DB 369 KKHAYCSNLSFRLYDQWRAMWQSKHTRNQDEGILPSGRGAARGPAG 416

RESULT 11

AAB19589

ID AAB19589 standard; protein; 407 AA.

XX AC

AAB19589;

XX XX

DT 22-JAN-2001 (first entry)

XX XX

Mouse cytokine-like factor-1.

XX DE

Cytokine-like factor-1; CLF-1; interleukin-B60; IL-B60; mouse; cytokine;
 receptor; neuron; inflammation; antiinflammatory; autoimmune disease;
 therapy.

XX OS

Mus musculus.

XX PN

WO200053631-A1.

XX XX

14-SEP-2000.

XX XX

09-MAR-2000; 2000WO-US006182.

XX PF

PR 11-MAR-1999; 99US-00267901.

XX XX

(SCHE) SCHERING CORP.

XX XX

Oppmann B, Timans JC, Kastelein RA, Bazan JF;

XX XX

WPI; 2000-587426/55.

DE Mouse cytokine receptor subunit NR7.
XX
KW DNAX cytokine receptor subunit 2; DCRS2; cell physiology;
KW cell development; cell culture; interferon detection;
KW immune system disorder; NR6; mouse.
XX
OS Mus sp.
XX
FN US2003082734-A1.
XX
PD 01-MAY-2003.
XX
PF 18-SEP-2002; 2002US-00247463.
XX
PR 01-JUN-1999; 99US-0137159P.
PR 31-MAY-2000; 2000US-00588113.
XX
PA (DOML/) DOWLING L M.
PA (TIMA/) TIMANS J C.
PA (GORM/) GORMAN D M.
PA (KAST/) KASTELEIN R A.
PA (BAZA/) BAZAN J F.
XX
PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan JF;
XX WPI; 2003-730048/69.
XX
DR Composition potentially useful for treating immunological disorders,
PT comprises a DNAX cytokine receptor subunit 2 (DCRS2) polypeptide, a
PT natural DCRS2 polypeptide, or a fusion polypeptide comprising a DCRS2
PT sequence.
XX
PS Disclosure; SEQ ID NO 5; 41pp; English.
XX
XX The invention describes a composition of matter (I) comprising a
CC substantially pure or recombinant DNAX cytokine receptor subunit 2
CC (DCRS2) polypeptide, a natural DCRS2 polypeptide, or a fusion protein
CC comprising a DCRS2 sequence. A composition of matter comprises: a
CC substantially pure or recombinant DCRS2 polypeptide comprising at least
CC three distinct nonoverlapping segments of at least four amino acids
CC identical to segments of a fully defined 384 amino acid sequence (S1),
CC given in the specification; a substantially pure or recombinant DCRS2,
CC polypeptide comprising at least two distinct nonoverlapping segments of
CC at least five amino acids identical to segments of S1; a natural sequence
CC DCRS2 comprising S1; or a fusion polypeptide comprising a DCRS2 sequence.
CC An agonist or antagonist of a mammalian DCRS2 is useful for modulating
CC physiology or development of a cell or cell culture. Antibodies to a
CC DCRS2 can be used for quantitative detection of interferon. The DCRS2
CC polypeptides and nucleic acids and their binding agents are potentially
CC useful in treating and diagnosing disease, especially disease associated
CC with the immune system. This is the amino acid sequence of mouse cytokine
CC receptor subunit NR6 used in a comparison with DCRS2.
XX
XX Sequence 407 AA;
SQ

Query Match 95.4%; Score 2209.5; DB 7; Length 407;
Best Local Similarity 99.8%; Pred. No. 1.7e-183;
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
1 RFLSSLSWSPLLLCVGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77
78 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLTAGSCLYVGLP 137
61 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLTAGSCLYVGLP 119
138 PKPFPNISCWSRNMKDLTCRWTFPGAGETFLHTNYSKYLKRWYGQDNTCEBYHTVGP 197
120 PKPFPNISCWSRNMKDLTCRWTFPGAGETFLHTNYSKYLKRWYGQDNTCEBYHTVGP 179
198 CHIPKDLALFTPYEIVWEATNRLGARSVDLFLDVLDDVVTTDPPPHVSRVGGLEDQLS 257

Db 180 CHIPKDLALFTPYEIVWEATNRLGARSVDLFLDVLDDVVTTDPPPHVSRVGGLEDQLS 239
QY 258 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLRLAGLKPGTVYFVQVR 317
Db 240 VRWVSPPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLRLAGLKPGTVYFVQVR 299
QY 318 PFGIYSGKAGIWSWSHPTAASSTPRSERPGGCGVCEPRGSGPSSGPVRRRELKQFLGWL 377
Db 300 PFGIYSGKAGIWSWSHPTAASSTPRSERPGGCGVCEPRGSGPSSGPVRRRELKQFLGWL 359
QY 378 KKHAYCSNLSPLRYDQWRAWMQKSHKTRNQDEGILPSSGRGAARGPAG 425
Db 360 KKHAYCSNLSPLRYDQWRAWMQKSHKTRNQDEGILPSSGRGAARGPAG 407
RESULT 14
ADT90845
ID ADT90845 standard; protein; 407 AA.
XX
AC ADT90845;
XX
DT 16-DEC-2004 (first entry)
XX
DE Mouse cytokine-like factor 1 (CLF-1).
XX
KW Interleukin; IL-B60; cytokine-like factor 1; CLF-1; CNTF-R;
KW CNTF-receptor; inflammatory condition; autoimmune disorder; mouse.
OS Mus sp.
XX
FN US2004192891-A1.
XX
PD 30-SEP-2004.
XX
PF 11-FEB-2004; 2004US-00778002.
XX
PR 11-MAR-1999; 99US-0124319P.
PR 09-MAR-2000; 2000US-00521335.
XX
PA (SCHE) SCHERING CORP.
XX
PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;
XX WPI; 2004-698788/68.
XX GENBANK; NM_004750.
XX Novel mammalian cytokines, useful for producing antigen-antibody complex,
PT treating conditions associated with abnormal physiology or development,
PT including inflammatory conditions and/or autoimmune disorders.
XX
PS Claim 1; SEQ ID NO 13; 41pp; English.
XX
CC The invention relates to a complex comprising interleukin (IL)-B60,
CC cytokine-like factor 1 (CLF-1) (partner sequence of IL-B60) and CNTF-R
CC (CNTF-receptor). The complex is useful for producing an antigen-antibody
CC complex, useful for treating conditions associated with abnormal
CC physiology or development, including inflammatory conditions and/or
CC autoimmune disorders and for generating antibodies which is useful in
CC diagnostic applications. The present sequence is mouse cytokine-like
CC factor 1 (CLF-1).
XX
SQ Sequence 407 AA;
Query Match 95.4%; Score 2209.5; DB 8; Length 407;
Best Local Similarity 99.8%; Pred. No. 1.7e-183;
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
18 RFLSSLSWSPLLLCVGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 77
1 RFLSSLSWSPLLLCVGVPRGGSGAHTAVISPDPTLLIGSSLOATCSIHGDTFGATAEGL 60
78 YWTLNGRRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLTAGSCLYVGLP 137

Db 61 YWTLNGRRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119
QY 138 PEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGODNTCEYHTVGP 197
Db 120 PEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGODNTCEYHTVGP 179
QY 198 CHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLTVDVTTDPPDVHVSRYVGGLEDQLS 257
Db 180 CHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLTVDVTTDPPDVHVSRYVGGLEDQLS 239
QY 258 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKPGTVYFVQVRCN 317
Db 240 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKPGTVYFVQVRCN 299
QY 318 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWL 377
Db 300 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 425
Db 360 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 407

RESULT 15

ADT61033
ID ADT61033 standard; protein; 407 AA.

AC ADT61033;

XX 16-DEC-2004 (first entry)

DE Mouse cytokine-like factor 1 (CLF-1).

XX Cytokine; interleukin-B60; IL-B60; cell physiology; immune system;
KW haematopoietic cell; immune disorder; T cell immune deficiency;
KW chronic inflammation; tissue rejection; cardiovascular condition;
KW neuropsychological condition; mouse; cytokine-like factor 1; CLF-1.

XX Mus sp.

XX US6800460-B1.

XX 05-OCT-2004.

XX 09-MAR-2000; 2000US-00521335.

XX 11-MAR-1999; 99US-0124319P.

XX (SCHE) SCHERING CORP.

XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;

XX WPI; 2004-697202/68.

XX New isolated or non-human host cells transfected with expression vectors
PT having nucleic acids encoding cytokines, useful in treating immune
PT disorders, cardiovascular or neuropsychological conditions.

XX Disclosure; SEQ ID NO 13; 37pp; English.

XX The invention relates to mammalian interleukin-B60 (IL-B60). The
CC invention also provides a method of producing a soluble complex
CC comprising the mature protein portions of IL-B60 and CLF-1 polypeptides.
CC The methods and compositions of the present invention are useful in
CC controlling biology and physiology of mammalian cells, such as cells of a
CC mammalian immune system, and in particular for regulating activation,
CC development, differentiation and function of various cell types,
CC including haematopoietic cells. They are specifically useful in treating
CC abnormal medical conditions, including immune disorders, such as T cell
CC immune deficiency, chronic inflammation or tissue rejection, or in
CC cardiovascular or neuropsychological conditions. The present sequence is
CC the mouse cytokine-like factor 1 (CLF-1).

XX

SQ Sequence 407 AA;
Query Match 95.4%; Score 2209.5; DB 8; Length 407;
Best Local Similarity 99.8%; Pred. No. 1.7e-183;
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 18 RPLSLMSPLLLICVLGVRGGSGAHTAVISPODPTLLIGSSLOATCSIHGDTGGATAGL 77
Db 1 RPLSLMSPLLLICVLGVRGGSGAHTAVISPODPTLLIGSSLOATCSIHGDTGGATAGL 60
QY 78 YWTLNGRRLPSLSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 137
Db 61 YWTLNGRRLPS-LSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 119
QY 138 PEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGODNTCEYHTVGP 197
Db 120 PEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGODNTCEYHTVGP 179
QY 198 CHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLTVDVTTDPPDVHVSRYVGGLEDQLS 257
Db 180 CHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLTVDVTTDPPDVHVSRYVGGLEDQLS 239
QY 258 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKPGTVYFVQVRCN 317
Db 240 VRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAGLKPGTVYFVQVRCN 299
QY 318 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWL 377
Db 300 PFGIYGSKKAGIWEWSHPTAASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWL 359
QY 378 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 425
Db 360 KKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGAARGPAG 407

Search completed: April 11, 2006, 02:09:55

Job time : 117.124 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: April 11, 2006, 02:10:19 ; Search time 21.2669 Seconds
(without alignments)
1922.808 Million cell updates/sec
Title: US-09-037-657-15
Perfect score: 2317
Sequence: 1 MFAGRPGVPAQARRPPRL.....NODEGILPSGRRGAARGPAG 425
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	331	14.3	288	B59405	prolactin receptor
2	331	14.3	376	A59405	prolactin receptor
3	331	14.3	622	A40144	prolactin receptor
4	329	14.2	918	A36337	membrane glycoprot
5	319.5	13.8	917	I49699	glycoprotein 130 -
6	317.5	13.7	918	A44257	interleukin-6 sign
7	314	13.6	830	I50455	prolactin receptor
8	312	13.5	310	A29884	prolactin receptor
9	312	13.5	412	A41070	prolactin receptor
10	312	13.5	610	A34631	lactogen receptor
11	312	13.5	610	A36116	prolactin receptor
12	307.5	13.3	292	I77525	prolactin receptor
13	307.5	13.3	303	I77524	prolactin receptor
14	307.5	13.3	608	I53269	prolactin receptor
15	307.5	13.3	616	A30304	prolactin receptor
16	306	13.2	831	JQ1655	prolactin receptor
17	302.5	13.1	581	I45971	prolactin receptor
18	261.5	11.3	630	I51086	prolactin receptor
19	254.5	11.0	771	B38252	granulocyte colony
20	254.5	11.0	783	JH0329	granulocyte colony
21	254.5	11.0	863	C38252	granulocyte colony
22	252.5	10.9	837	A34898	granulocyte colony
23	234	10.1	372	I58141	ciliary neurotroph
24	220.5	9.5	372	1 UHHUCN	ciliary neurotroph
25	209.5	9.0	422	I37891	interleukin-11 rec
26	208.5	9.0	432	I48343	interleukin-11 rec
27	208	9.0	362	S60614	growth promoting a
28	202.5	8.7	460	JL0145	interleukin-6 rece
29	200.5	8.7	468	A41242	interleukin-6 rece

30	199	8.6	156	2	A32868	prolactin receptor
31	194.5	8.4	440	2	JL0144	interleukin-6 rece
32	192.5	8.3	579	2	B45266	MPL-K protein prec
33	192.5	8.3	635	2	A45266	MPL-P protein prec
34	191.5	8.3	805	2	S68441	leptin receptor, s
35	191.5	8.3	892	2	S68439	leptin receptor, s
36	191.5	8.3	894	2	S68437	leptin receptor, s
37	191.5	8.3	900	2	S68440	leptin receptor, s
38	191.5	8.3	1162	2	S68438	leptin receptor, s
39	190	8.2	150	2	B34631	lactogen receptor
40	190	8.2	625	2	S35317	hematopoietic grow
41	190	8.2	1097	2	S17308	leukemia inhibitor
42	188.5	8.1	1162	2	PC4184	leptin receptor, O
43	186	8.0	626	2	S37622	proto-oncogene - m
44	185	8.0	1092	2	JX0312	differentiation-st
45	182	7.9	895	2	S74225	leptin receptor, i

ALIGNMENTS

RESULT 1

B59405

prolactin receptor short form Sib precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: B59405; B49400

R:Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin recep

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: B59405

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU>

A:Cross-references: UNIPROT:Q96P36; UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1

R:Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: B49400

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU2>

A:Cross-references: UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1

C:Comment: This is one of the short forms (Sla and Sib) of the human prolactin receptor ,

ta-casein gene promoter activation, with Sib more effective than Sla. However, their li

C:Genetics:

A:Gene: GDB:PLRL

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-288/Product: prolactin receptor, short form Sib #status predicted <NAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 331; DB 2; Length 288;

Best Local Similarity 37.5%; Pred. No. 3.7e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSCLVVG-LPPEKPFNISCSNRMDLTCRWTPGAGHGFLLHTNYSLKYKLWYQD 184

15 LFLNTCLLNGQLPPOKPEIFKCRSPNKETFFCWPRFGTDGG--LPTNLSLTHRGETILM 72

185 NTCSEYHTVGHPSCHIPKD-LALPTFPYBIWVEATNRLGARSDDLTLDLVDLVTTDPDPD 243

73 HECPDYITGGFNSCHFGKQYTSWRTYIMVNVNATWQSGSFSDLYVDVTYIVQDPDPLE 132

244 VHSRVGGLDQLSVRWV--SPALKDF---LFOAKYQIRYRVESVDWVKVDDVSNQTS 298

133 LAV-EVKQPEDRKPYLWIKNSPPTLIDLTGWTLLYELRLKPEKAEME-IHPAQQOTE 190

299 CRLAGLKPGTVYFVQVRCNPFGIYSGKKAGIWSHSPHTAASP 342

Db 191 FKLSLHPGQKYLQVQRCKP-----DHGYWSANSPATFIQIP 227

RESULT 2

A59405

prolactin receptor short form Sla precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: A59405; A49400

R:Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin receptor

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: A59405

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU>

A:Cross-references: UNIPROT:Q96P35; UNIPARC:UPI000006E673; GB:AF214012; PIDN:AF214012.1

R:Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: A49400

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU>

A:Cross-references: UNIPARC:UPI000006E673; GB:AF214012; PIDN:AF214012.1

C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor

eta-casein gene promoter activation, with S1a less effective than S1b. However, their li

ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: Sp13.3-Sp13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-376/Product: prolactin receptor, short form Sla #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 331; DB 2; Length 376;

Best Local Similarity 37.5%; Pred. No. 5.2e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSCLYVG-LPPEKPFNISCWSNMKDLTCRWTFGAHGETFLHTNYSLKYLKRWYQD 184

Db 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTVHREGETLM 72

QY 185 NTCEEYHTVGPCHSHPKD-LALFTPEYIWEATNRLGARSDDLTLVDLVDTVTPPPD 243

Db 73 HECPDYITGGNSCHFGKQYTSMWRTYIMVNATNQMGSSFSDELYVDVTVYIQDPDPLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYVEDSDVMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRKPYLWKWSPTLLDLKTGWFTLLYEIRLKPKEAAWE-IHFAGQQTE 190

QY 299 CRLAGLKPQTVYVQVRCNPFYIGSKKAGIWSHPTAASTP 342

Db 191 FKLSLHPGQKYLQVQRCKP-----DHGYWSANSPATFIQIP 227

RESULT 3

A40144

prolactin receptor long form precursor, hepatoma and breast cancer cells - human

C:Species: Homo sapiens (man)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C:Accession: A40144; A57018

R:Boutin, J.M.; Ederly, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.;

Mol. Endocrinol. 3, 1455-1461, 1989

A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human he

A:Reference number: A40144; MUID:90114212; PMID:2558309

A:Accession: A40144

A:Molecule type: mRNA

A:Residues: 1-622 <BOU>

A:Cross-references: UNIPROT:P16471; UNIPARC:UPI0000132234; GB:M31661; NID:g190361; PIDN:

R:Fuh, G.; Wellis, J.A.

J. Biol. Chem. 270, 13133-13137, 1995

A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li

A:Reference number: A57018; MUID:95286597; PMID:7768908

A:Accession: A57018

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 25-228, 'AW' <RES>

A:Cross-references: UNIPARC:UPI000006D208; GB:S78505; NID:g999114; PIDN:AAB34470.1; PID:

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: Sp13.3-Sp13.1

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-622/Product: prolactin receptor, long form #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.3%; Score 331; DB 2; Length 622;

Best Local Similarity 37.5%; Pred. No. 9.7e-18;

Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSCLYVG-LPPEKPFNISCWSNMKDLTCRWTFGAHGETFLHTNYSLKYLKRWYQD 184

Db 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTVHREGETLM 72

QY 185 NTCEEYHTVGPCHSHPKD-LALFTPEYIWEATNRLGARSDDLTLVDLVDTVTPPPD 243

Db 73 HECPDYITGGNSCHFGKQYTSMWRTYIMVNATNQMGSSFSDELYVDVTVYIQDPDPLE 132

QY 244 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYVEDSDVMKVVDDVSNQTS 298

Db 133 LAV-EVKQPEDRKPYLWKWSPTLLDLKTGWFTLLYEIRLKPKEAAWE-IHFAGQQTE 190

QY 299 CRLAGLKPQTVYVQVRCNPFYIGSKKAGIWSHPTAASTP 342

Db 191 FKLSLHPGQKYLQVQRCKP-----DHGYWSANSPATFIQIP 227

RESULT 4

A36337

membrane glycoprotein gp130 precursor - human

C:Species: Homo sapiens (man)

C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004

C:Accession: A36337

R:Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Cell 63, 1149-1157, 1990

A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.

A:Reference number: A36337; MUID:91084844; PMID:2261637

A:Accession: A36337

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-918 <HIB>

A:Cross-references: UNIPROT:P40199; UNIPARC:UPI0000046B12; GB:M57230; NID:g186353; PIDN:

C:Genetics:

A:Gene: GDB:IL6ST; GP130

A:Cross-references: GDB:126725; OMIM:600694

A:Map position: 5q11-5q11

C:Keywords: glycoprotein; membrane protein

F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 14.2%; Score 329; DB 2; Length 918;

Best Local Similarity 28.6%; Pred. No. 2.3e-17;

Matches 88; Conservative 51; Mismatches 151; Indels 18; Gaps 8;

QY 46 ISFPDPTLLIGSSLQATCSIHG---DTPGATAGLYWTNGRLRRLPELSRLNTSTLALA 102

Db 31 ISPESPVQLHNSFTAVCVLKEKCMDYFHVNANYIVMKTNHTFTPKEQYTIINRTASSVT 90

QY 103 LANLNGSRQSGDNLVCHARDGSLAGSLCYVGLPPEKPFNISCWSNMKDLTCRWTPGA 162

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Db 91 FTDIASLNTQLTCNLTITLQGLQONVYGITIIISGLPEKPKNLSCIVNEGKKRCRCEWDGGR 150
QY 163 HGETFLHTNYSKYKLRWYQDNTCEBYHTVGPSPHSGHCHIPKDLALFTPYBIWVEATNRLGS 222
Db 151 --ETHLETNFTLKSEWATHKPADCKAKRDT--PTSCITVDYSVYFVNIWVEAENALGK 206
QY 223 ARSDVLTLDLVDVVTDPDPVHVSXVGLGLEDQLSVRWVSPPALKDFLPQAKYQIRYRV 282
Db 207 VTSDHINFDPVYKVPNPNHLSVINSELSLTKLTWN-PSIKSVII-LKYNIOYRTK 264
QY 283 DSVDMKVV---DDVSNQTSCLAGIKPGTVYFVQVRCNPFPGIYGSKAGIWSWSHPTAA 339
Db 265 DASTWSQIPEDTASTRSSFTVQDLKPFTYEVFRIR-----MKEDGKGYNSDWSSEASG 319
QY 340 STPRSERP 347
Db 320 IT-YEDRP 326

RESULT 5
I49699
Glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I49699; I48370
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:192291532; PMID:1602143
A:Accession: I49699
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: UNIPROT:Q00560; UNIPARC:UPI000002845A; GB:M83336; NID:G193591; PIDN:
A:Accession: I48370
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: UNIPARC:UPI000002845A; EMBL:X62646; NID:G840816; PIDN:CAA44515.1; PI
C:Genetics:
C:Keywords: Glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 13.8%; Score 319.5; DB 2; Length 917;
Best Local Similarity 29.6%; Pred. No. 1.2e-16;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

QY 46 ISPODPTLLIGSSLQATCSIHG---DTPGATAEGLYWTILNGRRLPSELRLNTSTLALA 102
Db 31 IYPEPVPVQSGNFATCVLKEKACLOHYVNASYIVWKTNNHAAVPREQVTVINRTTSVT 90
QY 103 LANLNGSRQSGDNLVCHARDGSIILAGSLYVGLPPEKPFNISCWSRNKMDLTCRWTPGA 162
Db 91 FTDVVLPSVQLTCNLSFGQIEQNVYGVMTLSGFFPDKPTNLTCTIVNEGKNMLCQWDPCR 150
QY 163 HGETFLHTNYSKYKLRWYQD-NTCEEYHTVGPSPHSGHCHIPKDLALFTPYBIWVEATNRLG 221
Db 151 --ETYLETNYTLKSE--WATEKFPDQSKHGT---SCMVSYMTPTYYVNIWVEAENALG 203
QY 222 SARSDVLTLDVLDVVTDPDPVHVSXVGLGLEDQLSVRWVSPPALKDFLPQAKYQIRYRV 281
Db 204 KYSSSEINFPDVKVKPFPNMLSVTNSEELSLKLSWVSSGL--GGLDLKSDIQRT 261
QY 282 EDSVDWKVV---DDVSNQTSCLAGIKPGTVYFVQVRCNPFPGIYGSKAGIWSWSHPTA 338
Db 262 KDASTWIQVPLEDTWSPTSFTVQDLKPFTYEVFRIR----SIKDSGK-GYNSDWSSEAS 316
QY 339 AST--PRSERP 347
Db 317 GTTYEDRPSRP 327

RESULT 6
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44257
R:Wang, Y.; Neibitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin
A:Reference number: A44257; MUID:93052397; PMID:1427893
A:Accession: A44257
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8
A:Experimental source: liver
A>Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 317.5; DB 2; Length 918;
Best Local Similarity 29.8%; Pred. No. 1.8e-16;
Matches 92; Conservative 51; Mismatches 145; Indels 21; Gaps 10;

QY 46 ISPODPTLLIGSSLQATCSIHG---DTPGATAEGLYWTILNGRRLPSELRLNTSTLALA 102
Db 31 IYPEPVPVQSGNFATCVLKEKCLQVYSVNATYIVWKTNNHAAVPREQVTVINRTASSVT 90
QY 103 LANLNGSRQSGDNLVCHARDGSIILAGSLYVGLPPEKPFNISCWSRNKMDLTCRWTPGA 162
Db 91 FTDVVFQNVQLTCNLSFGQIEQNVYGITLSGYPDPDPTNLSCTIVNEGKNMLCQLDPCR 150
QY 163 HGETFLHTNYSKYKLRWYQD-NTCEEYHTVGPSPHSGHCHIPKDLALFTPYBIWVEATNRLG 221
Db 151 --ETYLETNYTLKSE--WATEKFPDQRTKH--GTSCMMGYPTIYFVNIWVEAENALG 204
QY 222 SARSDVLTLDVLDVVTDPDPVHVSXVGLGLEDQLSVRWVSPPALKDFLPQAKYQIRYRV 281
Db 205 NVSSEINFPDVKVKPFPNMLSVTNSEELSLKLAWSNGL--DSLRLKSDIQYRT 262
QY 282 EDSVDWKVV---DDVSNQTSCLAGIKPGTVYFVQVRCNPFPGIYGSKAGIWSWSHPTA 338
Db 263 KDASTWIQVPLEDTVSPRTSFTVQDLKPFTYEVFRIR----SIKENGK-GYNSDWSSE-BA 316
QY 339 ASTPRSERP 347
Db 317 SGTTYEDRP 325

RESULT 7
I50455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267; PMID:7516866
A:Accession: I50455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHS>
A:Cross-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:G466381; PIDN:
F:36-220/Domain: cytokine receptor homology <CRS>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 13.6%; Score 314; DB 2; Length 830;
Best Local Similarity 37.1%; Pred. No. 2.9e-16;
Matches 76; Conservative 29; Mismatches 82; Indels 18; Gaps 8;

QY 137 PPEKPFNISCWSRNKMDLTCRWTPGAHGTFLH-TNYSIKYKLRWYQDNTCEEYHTVGP 195
```


Db 231 PPEKFTIIKCRSPKETFTCWMPKSGDG---HPTNYTLTYSKEGEERVYECPDYKTAGP 287
Qy 196 HSCHI-PKDLALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTPPPDV--HVS RVGGL 252
Db 288 NSCYFDKHTSFWTYINIVKATNEIGNSVDPLVVDVYIVQTDPPFVNVVLELKKTVNR 347
Qy 253 EDQLSVRVSPALKDF---LFQAKYQIYRVVEDSDVKVVDVDSNQTSCRLAGLKPQTV 309
Db 348 KPYLVLTW-SPPLADRVSGMLTLDYELRLKPEAEWETI-FVQQTQHYKMFSLNPGCK 405
Qy 310 YFVQVRCNPFGLYGGKAGIWSWS 334
Db 406 YIVQIHCKP-----DHGHSWSEWS 424

RESULT 8
A29884
prolactin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
A:Accession: A29884
R:Boutin, J.M.; Jolicœur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A:Reference number: A29884; MUID:88165059; PMID:2832068
A:Accession: A29884
A:Molecule type: mRNA
A:Residues: 1-310 <BOU>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19A; GB:M19304; NID:g206364; PIDN:
C:Keywords: transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-310/Product: prolactin receptor #status predicted <MAT>
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 312; DB 2; Length 310;
Best Local Similarity 35.4%; Pred. No. 1.2e-16;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

Qy 125 SILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSLKYLKWYGD 184
Db 15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWNPFGTDGG--LPTNYSLTYSKE--GEK 65

Qy 185 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTPDP 241
Db 66 TTYECPDYKTSGPSNCFKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTYIVPEPEP 125

Qy 242 PDVHVSRYGLEDQLSVRWV--SPALKDF---LFQAKYQIYRVVEDSDVKVVDVDSNQ 296
Db 126 RNLT-L-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPBEAEWE-IHFTGHQ 183

Qy 297 TSCRLAGLKPQTVYFVQVRCNPFGLYGGKAGIWSWSHPTAATP 342
Db 184 TQKVPFDLYPGQKYLVTQCKP-----DHGWSRWSQESSVEMP 222

RESULT 9
A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
A:Accession: A41070; I55417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolact
A:Reference number: A41070; MUID:92041834; PMID:1718958
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN:
R:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor

A:Reference number: I55417; MUID:95014432; PMID:7929319
A:Accession: I55417
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: UNIPARC:UPI000002B19B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PI
A:Experimental source: Nb2-11C cell line
A:Keywords: transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 312; DB 2; Length 412;
Best Local Similarity 35.4%; Pred. No. 1.7e-16;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

Qy 125 SILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSLKYLKWYGD 184
Db 15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWNPFGTDGG--LPTNYSLTYSKE--GEK 65

Qy 185 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTPDP 241
Db 66 TTYECPDYKTSGPSNCFKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTYIVPEPEP 125

Qy 242 PDVHVSRYGLEDQLSVRWV--SPALKDF---LFQAKYQIYRVVEDSDVKVVDVDSNQ 296
Db 126 RNLT-L-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPBEAEWE-IHFTGHQ 183

Qy 297 TSCRLAGLKPQTVYFVQVRCNPFGLYGGKAGIWSWSHPTAATP 342
Db 184 TQKVPFDLYPGQKYLVTQCKP-----DHGWSRWSQESSVEMP 222

RESULT 10
A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
A:Accession: A34631
R:Zhang, R.; Buczko, B.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A:Reference number: A34631; MUID:90241201; PMID:2159291
A:Accession: A34631
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <ZHA>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170BE1; GB:M34083; NID:g205122; PIDN
A:Note: the authors translated the codon GAG for residue 533 as Gly
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 312; DB 2; Length 610;
Best Local Similarity 35.4%; Pred. No. 2.8e-16;
Matches 80; Conservative 35; Mismatches 85; Indels 26; Gaps 10;

Qy 125 SILAGSCLYVGLPPEKPFNISCWSRNKMDLTCRWTPGAHGETFLHTNYSLKYLKWYGD 184
Db 15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWNPFGTDGG--LPTNYSLTYSKE--GEK 65

Qy 185 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVVTTPDP 241
Db 66 TTYECPDYKTSGPSNCFKQYTSIWKIYIITVNATNQMGSSSDPLYVDVTYIVPEPEP 125

Qy 242 PDVHVSRYGLEDQLSVRWV--SPALKDF---LFQAKYQIYRVVEDSDVKVVDVDSNQ 296
Db 126 RNLT-L-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPBEAEWE-IHFTGHQ 183

Qy 297 TSCRLAGLKPQTVYFVQVRCNPFGLYGGKAGIWSWSHPTAATP 342
Db 184 TQKVPFDLYPGQKYLVTQCKP-----DHGWSRWSQESSVEMP 222

RESULT 11
A34116
prolactin receptor 2 precursor - rat

Db 206 ----DHGYWSRWGQEKSTIEP 222

RESULT 13

I77524

prolactin receptor precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C;Accession: I77524

R;Davis, J.A.; Linzer, D.I.H.

Mol: Endocrinol. 3, 674-680, 1989

A;Title: Expression of multiple forms of the prolactin receptor in mouse liver.

A;Reference number: I57699; MUID:89261824; PMID:2725531

A;Accession: I77524

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-303 <RES>

A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B197; GB:M22958; NID:g200479; PID:F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.3%; Score 307.5; DB 2; Length 303;

Best Local Similarity 32.6%; Pred. No. 2.6e-16;

Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

Qy 90 LSRLLNTSTLALANLANLNGSRQSGDNLVCHARDGSILAGSLYVGLPPEKPFNISCWSR 149

Db 1 MSSALAYMLVLVLSISLNG---QS-----PPGKEIHKCRSP 34

Qy 150 NMKDLTCRWTPGANGETFLHNYSLKYKLRWYGQNT--CBYHTVGPHSCHIPKD-LAL 206

Db 35 DKETFTCWNPQSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGNPCFPKQYTSI 90

Qy 207 FTPVEIWEATNRLGARSVDLTLDVLDVTTDPPDVHVSRVGGLDQLSVRWVS--PP 264

Db 91 WKYIIITVNATNMGSTSDPLYYVDVTVIVPEPPRNLT-L-EVKQLDKDKTYLWVKWLPP 149

Qy 265 ALKDF-----LFOAQIIRYRVSDVKVVDVDSNOTSCRLAGLKPGTVYFVQVRCNPFGI 321

Db 150 TIIDVTGKTFMTEVEIRLKSSEADEWE-IHTGHTQTFKVPFLYFGQKLVQTRCKP--- 205

Qy 322 YGSKKAGIWSHSHPTAATP 342

Db 206 ----DHGYWSRWGQEKSTIEP 222

RESULT 14

I53269

prolactin receptor, long form - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C;Accession: I53269; JT0671; S34356

R;Clarke, D.L.; Linzer, D.I.H.

Endocrinology 133, 224-232, 1993

A;Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.

A;Reference number: I53269; MUID:93307149; PMID:8319571

A;Accession: I53269

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-608 <RES>

A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020E90; GB:LI14811; NID:g293769; PID:R;Moore, R.C.; Oka, T.

Gene 134, 263-265, 1993

A;Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form

A;Reference number: JT0671; MUID:94085788; PMID:8262385

A;Accession: JT0671

A;Molecule type: mRNA

A;Residues: 1-608 <MOO>

A;Cross-references: UNIPARC:UPI0000020E90; GB:LI13593; NID:g347398; PIDN:AAC37641.1; PID:R;Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.

submitted to the EMBL Data Library, June 1993

A;Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.

A;Reference number: S34356

A:Accession: S34356
A:Molecule type: mRNA
A:Residues: 1-557,'F',559-608 <EDE>
A:Cross-references: UNIPARC:UPI0000163B24; EMBL:X73372; NID:G312696; PIDN:CAA51789.1; PI
C:Comment: Prolactin receptor have long form and short form which are resulted from alte
C:Comment: This long form receptor is capable of transducing a signal to milk protein ge
C:Keywords: receptor; transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>
F:230-253/Domain: transmembrane #status predicted <TMM>

Query Match 13.3%; Score 307.5; DB 2; Length 608;
Best Local Similarity 32.6%; Pred. No. 6.2e-16;
Matches 85; Conservative 37; Mismatches 92; Indels 47; Gaps 11;

QY 90 LSRLNLTSTLALANLNGSRQSGDNLVCHARDGSIILAGSLYVGLPPEKPFNISCWSR 149
DB 1 MSSALAYMLLVLSISILNG--QS-----PPGKPEIHKCRSP 34

QY 150 NMKDLTCRWTPGAHGETFLHTNYSLKYLRWYGQDNT--CEBYHTVGPHSCHIPKD-LAL 206
DB 35 DKETETCWNPNPGSDG--LPTNYSLTYSKE--GEKNTECPDYKTSGPNSCFFSKYQYTSI 90

QY 207 FFPYEIWEATNRLGARSDDLTLVDLVVTTDPPDVHVSRVGLEDQLSVRWVS--PP 264
DB 91 WKYIITVNATNMGSSSDPLVDVTVIIVEPEPRNLTL-EVKQKDKKTYLWVKWLP 149

QY 265 ALKDP---LFQAKYQIRYRVEDSVDMKVVDVSNQTSCLAGLKPCTVYFVQVRCNPFGI 321
DB 150 TITDVKTGFTWEYELRLKSEADEWE-IHFTGHQTOFKVFDLYPGQKLVQTRCKP--- 205

QY 322 YGSKKAGIWSWSHPTAASTP 342
DB 206 ----DHGYWSRWGQEKSIPI 222

RESULT 15
A30304
prolactin receptor 2 precursor - rabbit
N:Alternate names: prolactin receptor, mammary gland
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: A30304; A60380
R:Bedery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin,
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A:Title: Identification and sequence analysis of a second form of prolactin receptor by
A:Reference number: A30304; MUID:89184578; PMID:2928321
A:Accession: A30304
A:Molecule type: mRNA
A:Residues: 1-616 <EDE>
A:Cross-references: UNIPROT:P14787; UNIPARC:UPI0000132237; GB:J04510; NID:g165669; PIDN:
R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
Int. J. Biochem. 22, 1089-1095, 1990
A:Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto
A:Reference number: A60380; MUID:91146782; PMID:2289615
A:Accession: A60380
A:Molecule type: protein
A:Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108,150-164,'XX',167
A:Cross-references: UNIPARC:UPI000017C5D9; UNIPARC:UPI000017C5DA; UNIPARC:UPI000017C5DB;
C>Note: the amino end of the mature protein was blocked
C:Keywords: blocked amino end; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:235-258/Domain: transmembrane #status predicted <TMM>
F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.3%; Score 307.5; DB 2; Length 616;
Best Local Similarity 36.3%; Pred. No. 6.3e-16;
Matches 77; Conservative 28; Mismatches 90; Indels 17; Gaps 7;

QY 137 PPEKPFNISCWSRMKDLTCRWTPGAHGETFLHTNYSLKYLRWYGQDNTCEBYHTVGP 196
DB 27 PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNLTLYHKEGEITHECPDYKTGPGN 84

QY 197 SCHI-PKDLALFTPYEIVWEATNRLGARSDDLTLVDLVVTTDPPDVHVSRVGLEDQ 255
DB 85 SCYFSKKHTSIWTIYIITVNATNMGSSSDPRYVDVTVIIVEPDPFVNLTL-EVKHPEDR 143
QY 256 LSVRWVS--PPALKDQF---LFQAKYQIRYRVEDSVDMKVVDVSNQTSCLAGLKPCTVY 310
DB 144 KPYLWVKWLPPTLVDRSGWTLQYEIRLKEKAENE-THFAGQOTQFKILSLYPGQKY 202
QY 311 FVQVRCNPFGIYGSKKAGIWSWSHPTAASTP 342
DB 203 LVQVRCKP-----DHGFWSVWSPESSIQIP 227

Search completed: April 11, 2006, 02:17:25
Job time : 22.2669 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: April 11, 2006, 02:04:23 ; Search time 126.589 Seconds
 (without alignments)
 2368.694 Million cell updates/sec
 Title: US-09-037-657-15
 Perfect score: 2317
 Sequence: 1 MPAGRPGVQAQSRAPRPL.....NODEGILPSGRGAARGPAG 425

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2317	100.0	425	1 CRLP1_MOUSE	Q9Jm58 mus musculus
2	2176.5	93.9	422	1 CRLP1_HUMAN	O75462 homo sapien
3	1414.5	61.0	389	2 Q6G28_BRARE	Q6G28 brachydanio
4	1378.5	59.5	394	2 Q6UAQ5_TETNG	Q6uaq5 tetraodon n
5	995	42.9	437	2 Q4RMP5_TETNG	Q4rmp5 tetraodon n
6	468.5	20.2	207	2 Q4TCM7_TETNG	Q4tcm7 tetraodon n
7	416	18.0	151	2 Q4RDR1_TETNG	Q4rdr1 tetraodon n
8	380	16.4	199	2 Q4RDQ9_TETNG	Q4rdq9 tetraodon n
9	371	16.0	918	2 Q9W6U9_CHICK	Q9w6u9 gallus gall
10	355.5	15.3	881	2 O57519_XENLA	O57519 xenopus lae
11	332	14.3	268	2 Q8TD78_HUMAN	Q8td78 homo sapien
12	331	14.3	288	2 Q9GP36_HUMAN	Q9gp36 homo sapien
13	331	14.3	349	2 Q9UJH5_HUMAN	Q9uhj5 homo sapien
14	331	14.3	376	2 Q9GP35_HUMAN	Q9gp35 homo sapien
15	331	14.3	622	1 PRLR_HUMAN	P16471 homo sapien
16	331	14.3	622	2 Q5RAW0_PONPY	Q5raw0 pongo pygma
17	330.5	14.3	1010	2 Q7TQ89_RAT	Q7tq89 rattus norv
18	329	14.2	857	2 Q5FC04_HUMAN	Q5fc04 homo sapien
19	329	14.2	918	1 ILGRB_HUMAN	P40189 homo sapien
20	319.5	13.8	917	1 ILGRB_MOUSE	Q00560 mus musculus
21	319.5	13.8	917	2 Q6PD19_MOUSE	Q6pd19 mus musculus
22	317.5	13.7	918	1 ILGRB_RAT	P40190 rattus norv
23	316	13.6	622	2 Q9N0J7_CALJA	Q9n0j7 callithrix
24	314.5	13.6	608	2 Q99JZ1_MOUSE	Q99jz1 mus musculus
25	314	13.6	622	2 Q865V4_CEBAP	Q865v4 cebus apell
26	314	13.6	830	1 PRLR_COLLI	Q90374 columba liv
27	312	13.5	610	2 Q58DZ7_RAT	Q58dz7 rattus norv
28	312	13.5	610	1 PRLR_RAT	P05710 rattus norv
29	307.5	13.3	292	2 Q8C7G1_MOUSE	Q8c7g1 mus musculus
30	307.5	13.3	608	1 PRLR_MOUSE	Q08501 mus musculus
31	307.5	13.3	616	1 PRLR_RABIT	P14787 oryctolagus

32	307	13.2	625	1 PRLR_PIG	Q6jta8 sus scrofa
33	306	13.2	460	2 Q7T2Z0_CHICK	Q7t2z0 gallus gall
34	306	13.2	581	1 PRLR_SHEEP	O46561 ovis aries
35	306	13.2	831	1 PRLR_CHICK	O04594 gallus gall
36	306	13.2	831	2 Q6QDQ0_CHICK	Q6qdq0 gallus gall
37	305	13.2	831	1 PRLR_MELGA	Q91094 meleagris g
38	303	13.1	581	1 PRLR_CEREL	Q28235 cervus elap
39	302.5	13.1	581	1 PRLR_BOVIN	Q28172 bos taurus
40	294	12.7	611	2 Q9PTH9_XENLA	Q9pth9 xenopus lae
41	289.5	12.5	604	2 Q6UAP8_TETNG	Q6uap8 tetraodon n
42	289	12.5	357	2 Q4SQD8_TETNG	Q4sqd8 tetraodon n
43	289	12.5	819	2 Q616F7_EUBMA	Q616f7 eublepharis
44	288.5	12.5	611	2 Q91BF6_XENLA	Q91bf6 xenopus lae
45	288.5	12.5	611	2 Q9PTI0_XENLA	Q9pti0 xenopus lae

ALIGNMENTS

RESULT 1
 CRLP1_MOUSE
 ID CRLP1_MOUSE STANDARD; PRT; 425 AA.
 AC Q9Jm58;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)
 DE (CLP-1) (Cytokine receptor-like molecule 3) (CRLM-3) (NR6).
 GN Name=Crlf1; Synonyms=Crlm3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX PubMed10359701; DOI=10.1016/S0960-9822(99)80266-8;
 RA Alexander W.S., Raker S., Robb L., Farley A., Willson T.A.,
 Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,
 Hasegawa M., Maeda M., Fabri L., Jachno K., Nash A., Metcalf D.,
 Nicola N.A., Hilton D.J.;
 RT "Suckling defect in mice lacking the soluble haemopoietin receptor
 NR6.";
 RL Curr. Biol. 9:605-608(1999).
 [3]
 PHOSPHORYLATION SITE SER-222.
 RA Jin W.-H., Dai J., Zhou H., Xia Q.-C., Zou H.-P., Zeng R.;
 RT "Phosphoproteomic analysis of mouse liver using immobilized metal
 affinity purification and linear ion trap mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 18:2169-2176(2004).
 CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory
 role in the immune system and during fetal development. May be
 involved in nervous system development (by similarity). Plays an
 essential role in the initiation and/or maintenance of suckling in
 neonatal mice.
 CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a
 heteromeric complex with cardiotrophin-like cytokine (CLC); the
 CRLP1/CLC complex is a ligand for the ciliary neurotrophic factor
 receptor (CNTFR) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected
 in the brain of adult mice.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 folding and thereby efficient intracellular transport and cell-
 surface receptor binding.
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
 subfamily.
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 CC domain.
 CC -----

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----

CC EMBL; AB040038; BAA92777.1; -, mRNA.
 DR HSSP; P40223; 1CD9.
 DR Ensembl; ENSMUSG000000888; Mus musculus.
 DR MGI; MGI:1340030; Crfl1.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00835; IG-LIKE; FALSE NEG.
 KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
 KW Repeat; Signal.
 FT SIGNAL 1 33 Potential.
 FT CHAIN 34 425 Cytokine receptor-like factor 1.
 FT DOMAIN 35 134 Ig-like C2-type.
 FT DOMAIN 137 232 Fibronectin type-III 1.
 FT DOMAIN 237 337 Fibronectin type-III 2.
 FT MOTIF 330 334 WSXWS motif.
 FT MOD_RES 222 222 Phosphoserine.
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 107 107 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
 FT DISULFID 146 156 By similarity.
 FT DISULFID 187 198 By similarity.
 FT SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;
 CC -----

Query Match 100.0%; Score 2317; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 9.2e-175;
 Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRPGVAQARRPRPLSSLSWPLLCVLGVRGGSGAHTAVISPDPTLLIGSSILQ 60
 DB 1 MPAGRPGVAQARRPRPLSSLSWPLLCVLGVRGGSGAHTAVISPDPTLLIGSSILQ 60
 QY 61 ATCSIHGDTPGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 DB 61 ATCSIHGDTPGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
 QY 121 ARDGSILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW 180
 DB 121 ARDGSILAGSLYVGLPPEKPFNISCWRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW 180
 QY 181 YGQDNTCEEVHTVGPHSCHIPKDALFTPEYIWEATNRLGSARSDVLIDLVDDVTTP 240
 DB 181 YGQDNTCEEVHTVGPHSCHIPKDALFTPEYIWEATNRLGSARSDVLIDLVDDVTTP 240
 QY 241 PPDVHVSRRVGGLEDQLSVRWVSPALKDFLQAKYQIRYRVDSVDKVVDDVSNQTSR 300
 DB 241 PPDVHVSRRVGGLEDQLSVRWVSPALKDFLQAKYQIRYRVDSVDKVVDDVSNQTSR 300
 QY 301 LAGLKEGTGVYFQVRCNPFGIYSGKKAGIWESEHSPTAASRPSRPGGGVCEPRGGE 360
 DB 301 LAGLKEGTGVYFQVRCNPFGIYSGKKAGIWESEHSPTAASRPSRPGGGVCEPRGGE 360
 QY 361 PSSGPVRRRELKQFLGWLKHHAYCSNLSPFLYDQRAWMQSHKTRNQDEGILPSGRGAA 420
 DB 361 PSSGPVRRRELKQFLGWLKHHAYCSNLSPFLYDQRAWMQSHKTRNQDEGILPSGRGAA 420
 QY 421 RGPAG 425

Db 421 RGPAG 425

|||||

RESULT 2

CRFL1 HUMAN

ID CRFL1_HUMAN STANDARD; PRT; 422 AA.
 AC Q75462; O9UHS;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)
 DE (CLF-1) (Zcytor5).
 GN Name=CRFL1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 RN NCBI_TaxID=9606;
 RX [1]
 RP NUCLEOTIDE SEQUENCE, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, AND INDUCTION.
 RC TISSUE=Fetal lung;
 RX MEDLINE=98349389; PubMed=9686600;
 RA Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,
 RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;
 RT "Cytokine-like factor-1, a novel soluble protein, shares homology with
 RT members of the cytokine type I receptor family.";
 RL J. Immunol. 161:1371-1379(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Magrangeas F., Jacques Y., Minvielle S.;
 RT "Cloning and expression of a novel soluble protein containing
 RT hemopoietic cytokine receptor domains.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Lok S., Preenell S.R., Jellmberg A.C., Gilbert T., Whitmore T.E.,
 RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
 RA Vansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP PROTEIN SEQUENCE DOI=38-52.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [7]
RP INTERACTIONS WITH CLC AND CNTRF.
RX MEDLINE=20423191; PubMed=1096616; DOI=10.1038/78765;
RA Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau H.,
RA Frogier J., Suard I., de Coignac A.B., Delneste Y., Bonnefoy J.Y.,
RA Gauchat J.-F., Gascan H.;
RT "CLF associates with CLC to form a functional heteromeric ligand for
RT the CNTRF receptor complex.";
RL Nat. Neurosci. 3:867-872(2000).
RN [8]
RP VARIANTS CISS HIS-81 AND ARG-374.
RX MEDLINE=22428294; PubMed=12509788;
RA Knappskog P.M., Majewski J., Livneh A., Nilsen P.T.E., Bringsli J.S.,
RA Ott J., Bonan H.;
RT "Cold-induced sweating syndrome is caused by mutations in the CRLF1
RT gene.";
RL Am. J. Hum. Genet. 72:375-383(2003).
CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory
CC role in the immune system and during fetal development. May be
CC involved in nervous system development.
CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a
CC heteromeric complex with cardiotrophin-like cytokine (CLC); the
CC CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor
CC receptor (CNTRF).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highest levels of expression observed in
CC spleen, thymus, lymph node, appendix, bone marrow, stomach, in
CC placenta, heart, thyroid and ovary. Strongly expressed also in
CC fetal lung.
CC -!- INDUCTION: Up-regulated in fibroblast primary cell cultures under
CC stimulation by IFN-gamma, TNF-alpha and IL-6.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -!- DISEASE: Defects in CRLF1 are the cause of cold-induced sweating
CC syndrome (CISS) [MIM:272430]. CISS is an autosomal recessive
CC disorder characterized by profuse sweating induced by cool
CC surroundings (temperatures of 7 to 18 degrees Celsius). Additional
CC abnormalities include a high-arched palate, nasal voice, depressed
CC nasal bridge, inability to fully extend the elbows and
CC kyphoscoliosis.
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
CC subfamily.
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF059293; AAC28335.1; -; mRNA.
CC EMBL; AF073515; AAD39681.1; -; mRNA.
CC EMBL; AF178684; AAD54385.1; -; mRNA.
CC EMBL; AY358291; AAQ88658.1; -; mRNA.
CC EMBL; BC044634; AAH44634.1; -; mRNA.
CC HSSP; P40223; 1CD9.

DR Ensembl; ENSG00000006016; Homo sapiens.
DR HGNC; HGNC:2364; CRLF1.
DR MIM; 604237; -.
DR MIM; 272430; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0019955; P:cytokine binding; IPI.
DR GO; GO:0004872; P:receptor activity; TAS.
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. .); TAS.
DR InterPro; IPR002996; Cytokn recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF000411; fn3; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
KW Direct protein sequencing; Disease mutation; Glycoprotein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.
FT SIGNAL 1 37
FT CHAIN 38 422 Cytokine receptor-like factor 1.
FT DOMAIN 38 131 Ig-like C2-type.
FT DOMAIN 134 229 Fibronectin type-III 1.
FT DOMAIN 224 334 Fibronectin type-III 2.
FT MOTIF 327 331 WSXWS motif.
FT MOD_RES 219 219 Phosphoserine (By similarity).
FT CARBOHYD 92 92 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 140 140 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 382 382 N-linked (GlcNAc. .) (Potential).
FT DISULFID 143 153 By similarity.
FT DISULFID 184 195 By similarity.
FT VARIANT 81 81 R -> H (in CISS).
FT VARIANT 374 374 L -> R (in CISS).
FT CONFLICT 240 240 /FTID=VAR_017865.
FT CONFLICT 240 240 /FTID=VAR_017866.
FT CONFLICT 240 240 D -> E (in Ref. 3).
SQ SEQUENCE 422 AA; 46302 MW; AD9DFCB01B84228 CRC64;
Query Match 93.9%; Score 2176.5; DB 1; Length 422;
Best Local Similarity 94.8%; Pred No. 1.2e-163;
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;
QY 1 MPAGRPGVPAQSARPPRLSLSLSPLLCVLGVPRGSGAHTAVISPODPTLLIGSSLQ 60
DB 1 MPAGRPGPAQSARPP-PLLP-LL-LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSL 57
QY 61 ATCSIHGDTPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDPGATAGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNTSLKYKLAW 180
DB 118 ARDGSILAGSCLYVGLPPEKPNISCSNRNMKDLTCRWTPGAHGETFLHTNTSLKYKLAW 177
QY 181 YQDNTCEYHTVGPFSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDLVVTTDP 240
DB 178 YQDNTCEYHTVGPFSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDLVVTTDP 237
QY 241 PPDVHVSRVGGLEDQLSVRWVSPALKKDFLFOAKYQIRYRVEDSVDKVDDVSNQTSR 300
DB 238 PPDVHVSRVGGLEDQLSVRWVSPALKKDFLFOAKYQIRYRVEDSVDKVDDVSNQTSR 237
QY 301 LAGLXPGTVYFVQVRCNPGIYGSKKAGIWSWSHPTAASTPRSRPGGVCPRGG 360
DB 298 LAGLXPGTVYFVQVRCNPGIYGSKKAGIWSWSHPTAASTPRSRPGGVCPRGG 357
QY 361 PSSGPRRELKQFLGWLKKHAYCSNLSFLYDQWRAMQSHKTRNQDEGILLPSGRGAA 420
DB 358 PSSGPRRELKQFLGWLKKHAYCSNLSFLYDQWRAMQSHKTRNQDEGILLPSGRGAA 417
QY 421 RQPA 424
DB 418 RGPA 421

```

RESULT 3
Q6DG28 BRARE PRELIMINARY; PRT; 389 AA.
ID Q6DG28 BRARE PRELIMINARY; PRT; 389 AA.
AC Q6DG28
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Zgc:91992.
GN ORFNames=zgc:91992;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gichmond J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherth A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC EMBL; BC076526; AAH76526.1; -; mRNA.
DR ZFIN; ZDB-GENE-040718-397; zgc:91992.
DR InterPro; IPR002996; CytKn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
KW Receptor; Repeat; Transmembrane.
SQ SEQUENCE 389 AA; 43314 MW; E30903B99639864A CRC64;

Query Match 61.0%; Score 1414.5; DB 2; Length 389;
Best Local Similarity 68.1%; Pred. No. 2.1e-103;
Matches 260; Conservative 48; Mismatches 67; Indels 7; Gaps 5;

QY 27 LLLCVLGVPRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDPGATAGLYWTLNGRRL 86
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
7 LHLCAAGVL--SSSTQVATIPQDPALLIGSSILATCSVNPDP-HGIHAGSLYWTLNGKRL 63
QY 87 PSELRLTLTSTLALANLNGSRQSGDNLVCHARDGSLAGSLCYVGLPPEKPNISC 146
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 PSSTYSLSPTVISVTLPLRLSGRQRSGDNLVCHNGGHLVAGSLCYVGMPPKPNLTC 123
QY 147 WSNRMKDLTCRWTPGAHGETFLHTNYSLKYKLWYGQDNTCEBYHTVGPHSCHI PKDAL 206
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 WSRNTKDLICRWAPGQGETFIKTKYTLKYLWYGREKECEDYSTGEPTCYIPRDLAL 183

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QY 207 FTPYEIWEATRLGARSDDLTLVDLVVTTDPDPDVHVSRLVGGLEDOLSVRWVSPRAL 266
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 FTPYEIWEASNLQGTATSDIYLDVTTDPDTVTVSRLVGGLEDOLTVRWGTPPAL 243
QY 267 KDFLFQAKYQIRYRVEDSDVKVVDVDSNOTSRLAGLKPQTVYFVQVRCNPFYIGSKK 326
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 KDFLFQAKYQIRYRLSESDVKVVDVDSNOTSRLAGLPGTVYFVQVRCNPFYIGLSRK 303
QY 327 AGIWSHSHPTAASTRSRPQGGVCEPRGEPSSGVRRELKQFLGWLKKHAY-CSN 385
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 AGIWSHSHPTAASTRSRPQGGVCEPRGEPSSGVRRELKQFLGWLKKHAY-CSN 360
QY 386 LSFRLYDQRAWQKSHKTRNQ 407
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 MSIKLYDQRAWVWLQKSHKTRNQ 382

RESULT 4
Q6UAQ5 TETNG PRELIMINARY; PRT; 394 AA.
ID Q6UAQ5 TETNG PRELIMINARY; PRT; 394 AA.
AC Q6UAQ5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Class I helical cytokine receptor number 1.
GN Name=CRPAL;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Maucell E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicad S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Binmont C., Skalli Z., Cattolico L., Poulain J., Berardinis Vd.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Guzy J.,
RA Farra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigs R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quittier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Crolius H.R.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC EMBL; AY374473; AAR25664.1; -; mRNA.
DR Ensembl; AY374473; Tetraodon nigroviridis.
DR GO; GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR002996; CytKn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Receptor; Repeat; Transmembrane.
SQ SEQUENCE 394 AA; 44022 MW; EE60B16FA2C2896C CRC64;

Query Match 59.5%; Score 1378.5; DB 2; Length 394;
Best Local Similarity 67.6%; Pred. No. 1.5e-100;
Matches 259; Conservative 39; Mismatches 80; Indels 5; Gaps 4;

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QY 27 LLLCVLGVPRG-GSGAHTAVISQDPTLLIGSSLOATCSIHGDTFGATAGSLYWTNLGRR 85
 DB 9 LLLLLHSPAVLALSTHVAIVYQDPVLRMGSNLTASCWIRSD-L-GVHASSLFWTLNGQP 67
 QY 86 LPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNIS 145
 DB 68 LPSSLRVLSFTNLVTLAGLNARQTSQGNLVCHHKGHLAGSCLYVGMPPAKPVNLT 127
 QY 146 CWSERNKMDLFCRWTPGAHGTFTLHTNYSKYKLRWYGQDNTCEBYHTVGPHSCHIPKDLA 205
 DB 128 CWSERNKMDLFCRWTPGAHGTFTLHTNYSKYKLRWYGQDNTCEBYHTVGPHSCHIPKDLA 187
 QY 206 LFTPEYIWEATNRLGSRDVLTLVDVLTDPDPDVHVRVGGLEDQLSVRWVSPPA 265
 DB 188 LFTPEYIWEATNRLGSRDVLTLVDVLTDPDPDVHVRVGGLEDQLSVRWVSPPA 247
 QY 266 LKDFLPQAKYQIRVRVEDSVWVDDVNSQTSRLAGLPGTVYFVQVRCNPPGYGSK 325
 DB 248 LKDFLPQAKYQIRVRVEDSVWVDDVNSQTSRLAGLPGTVYFVQVRCNPPGYGSK 307
 QY 326 KAGIWESEWHSPTAASPRSRPGGVCPEPRGSPSSGPRRELKQFLGWLKXKAY-CS 384
 DB 308 KAGIWESEWHSPTAASPRSRPGGVCPEPRGSPSSGPRRELKQFLGWLKXKAY-CS 365
 QY 385 NLSFRLYDQWRWQKSHKTRNQ 407
 DB 366 SMSMKLYDQWRWQKSHKTRNQ 388

RESULT 5

Q4RMP5_TETNG
 ID Q4RMP5_TETNG PRELIMINARY; PRT; 437 AA.
 AC Q4RMP5;
 DT 13-SEP-2005 (TEMBLrel. 31, Created)
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE Chromosome 10 SCAF15019, whole genome shotgun sequence.
 DE (Fragment).
 DE ORFNames=GSTENG00031935001;
 GN Tetraodon nigroviridis (Green puffer).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01015019; CAG10337.1; -; Genomic_DNA.
 FT NON TER 1 1
 SQ SEQUENCE 437 AA; 49065 MW; 99F9602E88F95583 CRC64;

Query Match 42.9%; Score 995; DB 2; Length 437;
 Best Local Similarity 53.8%; Pred. No. 3.9e-70;
 Matches 199; Conservative 33; Mismatches 62; Indels 76; Gaps 5;
 QY 44 AVISPODPTLLIGSSLOATCSIHGDTFGATAGSLYWTNLGRRPSELRLNTSTLAL 103
 DB 1 AVIYQDPVLRMGSNLTASCWIRSD-L-GVHASSLFWTLNGQPLPSSLYRVLSPTNLSVTL 59
 QY 104 ANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNIS 163
 DB 60 AGLNARQTSQGNLVCHHKGHLAGSCLYVGMPPAKPVNLT-CWSRNKMDLTCWAPGGR 119
 QY 164 GETFLHTNYSKYKLRWYGQDNTCEBYHTVGPHSCHIPKDLAFTPEYIWEATNRLGSA 223
 DB 120 GETHISTQVTLKYKLRWYGKECEDYTHVQVYSCSITRDLHLFTPEYIWEATNRLGSA 179
 QY 224 RSDVLTDLVDVLTDPDPDVHVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRVRVED 283
 DB 180 TSDVITLIDLVDVLTDPDPDVHVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRVRVED 239
 QY 284 SVDWK-----VVDD 292
 DB 240 SQDWKEKSAFDOERERANTEPLCILGLRVLMNEKYSVEAGPLQMALRLILLPVLWVDD 299
 QY 293 VSNQTSRLAGLPGTVYFVQVRCNPPGYGSKKAG-----IWSHSPHTAASPRSRPG 348
 DB 300 VGNQTSRLAGLPGTVYFVQV-----GPRSSASDRIMI-----SDRRV 339
 QY 349 PGGGVCEPRG 358
 DB 340 ASAGPLQPRG 349

RESULT 6

Q4TCM7_TETNG
 ID Q4TCM7_TETNG PRELIMINARY; PRT; 207 AA.
 AC Q4TCM7;
 DT 13-SEP-2005 (TEMBLrel. 31, Created)
 DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF6801, whole genome shotgun sequence.
 DE (Fragment).
 DE ORFNames=GSTENG00003230001;
 GN Tetraodon nigroviridis (Green puffer).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McSwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.


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DR EMBL; CAAE01006801; CAF89355.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 22607 MW; 71F8E80B9998309F CRC64;

Query Match 20.2%; Score 468.5; DB 2; Length 207;
Best Local Similarity 48.3%; Pred. No. 6.9e-29;
Matches 102; Conservative 7; Mismatches 21; Indels 81; Gaps 4;

QY 231 DVLVDVTTDPPDVHVSRRVGGLEDQLSVRWVSPALDKFLFOAKYQIRYRVDSVDWK-- 288
D 1 ECLPVTTPDPPSGTVSVRVGQLEDQLSVRWVSPALDKFLFOAKYQIRYRVDSVDWKKE 60
QY 289 -----VVDVNSQITSC 299
D 61 KSAFQDERAWTEPLCILGLRLVMNEKYSVEAGPLQMALRLILLPVLVWMDVNGQITSC 120
QY 300 RLAGLKPGTVY-----FVQVRCNPGIYSGKKAGIWSWSHPT 337
D 121 RLAGLRPGTVYSRWDPVPAPQOTGSGSLTAVSLPQVRCNPGIYSGRKAGIWSWSHPT 180
QY 338 AASTPRSERP----GRGGVCEPRGGEPSG 364
D 181 AASTPHSGEPPLPAGPGRSL----GSAPESG 207

RESULT 7
Q4RDR1 TETNG
ID Q4RDR1 TETNG PRELIMINARY; PRT; 151 AA.
AC Q4RDR1
DT 13-SEP-2005 (TREMREL. 31, Created)
DT 13-SEP-2005 (TREMREL. 31, Last sequence update)
DT 13-SEP-2005 (TREMREL. 31, Last annotation update)
DE Chromosome undetermined SCAF15947, whole genome shotgun sequence.
GN ORFNames=GSTENG00037335001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01015948; CAG13473.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 199 AA; 21734 MW; 299786CDFB24BDEB CRC64;

Query Match 16.4%; Score 380; DB 2; Length 199;
Best Local Similarity 67.0%; Pred. No. 6.6e-22;
Matches 73; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

QY 236 VTTDPPDPVHVSRRVGGLEDQLSVRWVSPALDKFLFOAKYQIRYRVDSVDWKVDDVSN 295
D 34 VTTDPTDVHVSRRVGGLEDQLTVRWTSPDLEILFOAKYQIRYRVDSVDWKVDDVSN 87
QY 296 QTSCLAGLPGTVYFVQVRCNPGIYSGKKAGIWSWSHPTAASPTPS 344
D 88 -----SVLWTVHFVQVRCNPGIYSGRKAGIWSWSHPTAASPTPS 128

RESULT 9
Q9WEU9_CHICK

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ID Q9W6U9_CHICK PRELIMINARY; PRT; 918 AA.
 AC Q9W6U9;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Glycoprotein 130 precursor.
 GN Name=gpi30;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryonic heart primary culture;
 RX MEDLINE=99026068; PubMed=9806927;
 RA Geissen M., Heller S., Pennica D., Ernberger U., Rohrer H.;
 RT "The specification of sympathetic neurotransmitter phenotype depends
 on gpi30 cytokine receptor signaling.";
 RL Development 125:4791-4801(1998).
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 folding and thereby efficient intracellular transport and cell-
 surface receptor binding (By similarity).
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 activation (By similarity).
 DR EMBL; AJ011688; CAB42084.1; -; mRNA.
 DR HSSP; P40189; 1BQU.
 DR InterPro; IPR002996; Cytok_recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003529; Hemtrecept_1302.
 DR InterPro; IPR010457; Lep_receptor_Ig.
 DR Pfam; PF00041; fn3; 4.
 DR Pfam; PF06328; Lep_receptor_Ig; 1.
 DR SMART; SM00060; FN3; 4.
 DR PROSITE; PS00853; FN3; 5.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 SQ SEQUENCE 918 AA; 102495 MW; FE7625FF3E3613BF CRC64;

 Query Match 16.0%; Score 371; DB 2; Length 918;
 Best Local Similarity 30.2%; Pred. No. 2.4e-20;
 Matches 111; Conservative 41; Mismatches 138; Indels 78; Gaps 16;

 QY 27 LLLCVLGVPRGSGAHTAVISQDPTLLIGSSIQATCSIHG---DTPGATAGLYWTLNG 83
 DB 16 LNICFEV--SGGLVSCGHIIPESVLAGSNFTALCILNESCLDFGNIIYASQIIWKMN 74

 QY 84 RRLPSLSRLN-----TSTLALANLNGSRQSGDNLVCHA-RDGSI---LAG 129
 DB 75 KVIPKEQYREINRTVSSVTFNDTSSLA-----SPLTCNVLDAGQIEQNIYG 120

 QY 130 SCLYGLPPEKPFNISC-----WSNMKDLTCRWTPGAGHGTFLHTNYSLKYLKRW 180
 DB 121 ISVTVGLPPEKPNLSICVYLSPKVEWYNN-----CTWNPGRH--TFLDTRFLKYMWR 173

 QY 181 YQDNTCEHYTVGHSCHI PKDALFTPYEIVWEATNRLGARSQDVLTLVDLVVTTDP 240
 DB 174 ETPFPCIPYVN---NSCTI--SDVOFFVNLEWVVEAANALGAESDHLVDFDIEIVKPP 229

 QY 241 PPDVHVSRRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVQKVV---DVSNOT 297
 DB 230 PRLNSVNS--GILPTVLKLSWEN--QISTVVMELKNIRYRISDYNWMEVPEDTASPT 286

 QY 298 SCRLAGLKPQTVYVQVRCNPFYIGSKKAGIWSWSHPTAASRPRSRPGRPGGVCBPR 357
 DB 287 SPSIQGLRPTVYVFSIRC-----NKEDGVGFWSWSEIRQIGVTTED----- 328

 QY 358 GGEPSGP 365
 DB 329 --KPSKGP 334

RESULT 10
 ID 057519_XENLA PRELIMINARY; PRT; 881 AA.
 AC 057519;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Gp130p1.
 GN Name=xgp130;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Chen J., Grace A., Chien K.R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 folding and thereby efficient intracellular transport and cell-
 surface receptor binding (By similarity).
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
 activation (By similarity).
 DR EMBL; AF041845; AAC03531.1; -; mRNA.
 DR HSSP; P40189; 1BQU.
 DR InterPro; IPR002996; Cytok_recept_B/G.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003529; Hemtrecept_1302.
 DR InterPro; IPR010457; Lep_receptor_Ig.
 DR Pfam; PF00041; fn3; 4.
 DR Pfam; PF06328; Lep_receptor_Ig; 1.
 DR SMART; SM00060; FN3; 4.
 DR PROSITE; PS00853; FN3; 5.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 KW Receptor; Repeat; Transmembrane.
 SQ SEQUENCE 881 AA; 99003 MW; 7DB7942D211138A0 CRC64;

 Query Match 15.3%; Score 355.5; DB 2; Length 881;
 Best Local Similarity 30.5%; Pred. No. 3.8e-19;
 Matches 100; Conservative 43; Mismatches 136; Indels 49; Gaps 11;

 QY 50 DPTLLIGS-SLOATCSIHGDTFGATAGLYWTLNGRRLPSELSRLNTSTLALANLNG 108
 DB 33 DRGIVHGERPPTAYCVINQTCRLREDASRIYVLVKGKVPETQVTEILLNQTTSSVTPENLT 92

 QY 109 SRQSGDNLVCHARGDSILAGSLYGLPPEKPFNISCWSNMKDLTCRWTPGAGHGTFL 168
 DB 93 LNSPLTCNVMSAGHVANTLYGIFFTGLPDPKPTNLTCIVYNQDNLTCWDFGR--PTNL 150

 QY 169 HTNYSLKYLKRW-----YQDNTCEHYTVGHSCHI PKDALFTPYEIVWEATNRL 220
 DB 151 PNTYLSH--RWAHFGANYCRGANNSC-----THSP-GFQFYIDTTQVEATNRL 198

 QY 221 GSARSDVLTLDLVDTVVTPDPDVHVSRRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYR 280
 DB 199 GIQKSETLITDPNVNKPENPPQLSELISSELPNALKIEWKNPIT---NAFNLYNIRYR 255

 QY 281 VEDSVQKVV---DVSNOTSCRLAGLKPQTVYVQVRCNPFYIGSKKAGIWSWSHPT 337
 DB 256 PVKTDQWEMVPEDTASHRDSFTLQDLPLNTYVYSIRC-----IHKDGHGFWSWSELK 310

 QY 338 AASTPRSRPGRPGGVCPRGGEPSGP 365
 DB 311 KQVTP--EAP-----PSRGP 323

 RESULT 11
 Q8TD78_HUMAN
 ID Q8TD78_HUMAN PRELIMINARY; PRT; 268 AA.
 AC Q8TD78;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```
DE Prolactin receptor delta 7/11.
OS Homo sapiens (Human)
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast tumor;
RA Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AF492470; AAM18048.1; -, mRNA.
DR HSSP; P16471; 1BP3.
DR SMR; Q8TD78; 29-227.
DR Ensembl; ENSG00000113494; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytnk_recept_E/G.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 268 AA; 30705 MW; FBB498AB649A078C CRC64;

Query Match 14.3%; Score 332; DB 2; Length 268;
Best Local Similarity 37.0%; Pred. No. 6.1e-18;
Matches 84; Conservative 28; Mismatches 97; Indels 18; Gaps 8;

QY 126 ILAGSLCYVG-LPPEKPFNISCWRNMKDLTCRWTPGAGHETFLHTNYSKYLKRWYGD 184
DB 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPTDGG--LPTNYSLTVHREGETLM 72
QY 185 NTCSEYHTVGHPSCHIPKD-LALFTPEYIWEVATNRLGARSADVLTLDVLDVTTDPPD 243
DB 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQMGSSFSDELVDVYIVQPPPLE 132
QY 244 VHSVRVGGLEDQLSVRWV--SPALKDFF--LFOAKYQIRYRVDSVDMKWVDVDSNQS 298
DB 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYEIRLPEKAAWE-IHFAGQQT 190
QY 299 CRLAGLPGTVYFVQVRCNPFGIYSGKKAGIWSWSHPTAASTP 345
DB 191 FKLSLHPGQKYLQVQRCKP-----DHGYSAWSPATFIQIPSGD 230

RESULT 12
Q96P36 HUMAN
ID Q96P36 HUMAN PRELIMINARY; PRT; 288 AA.
AC Q96P36;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prolactin receptor short isoform 1b.
GN Name=PRLR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RX PubMed=11518703;
RA Hu Z.Z., Meng J., Dufau M.L.;
RT "Isolation and characterization of two novel forms of the human
RT prolactin receptor generated by alternative splicing of a newly
RT identified exon 11."
RL J. Biol. Chem. 276:41086-41094 (2001).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
DR EMBL; AF416618; AAL23914.1; -, mRNA.
DR PIR; B59405; B59405.
DR HSSP; P16471; 1BP3.
DR SMR; Q96P36; 29-227.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytnk_recept_E/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtrecept_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 288 AA; 32760 MW; B45203EC045EB417 CRC64;

Query Match 14.3%; Score 331; DB 2; Length 288;
Best Local Similarity 37.5%; Pred. No. 8e-18; 95; Indels 18; Gaps 8;
Matches 84; Conservative 27; Mismatches 95; Indels 18; Gaps 8;

QY 126 ILAGSLCYVG-LPPEKPFNISCWRNMKDLTCRWTPGAGHETFLHTNYSKYLKRWYGD 184
DB 15 LFLNTCLLQGLPPGKPEIFKCRSPNKETFTCWRRPTDGG--LPTNYSLTVHREGETLM 72
QY 185 NTCSEYHTVGHPSCHIPKD-LALFTPEYIWEVATNRLGARSADVLTLDVLDVTTDPPD 243
DB 73 HECPDYITGPNSCFHGKQYTSWRTYIMMVNATNQMGSSFSDELVDVYIVQPPPLE 132
QY 244 VHSVRVGGLEDQLSVRWV--SPALKDFF--LFOAKYQIRYRVDSVDMKWVDVDSNQS 298
DB 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYEIRLPEKAAWE-IHFAGQQT 190
QY 299 CRLAGLPGTVYFVQVRCNPFGIYSGKKAGIWSWSHPTAASTP 342
DB 191 FKLSLHPGQKYLQVQRCKP-----DHGYSAWSPATFIQIP 227

RESULT 13
Q9UHJ5 HUMAN
ID Q9UHJ5 HUMAN PRELIMINARY; PRT; 349 AA.
AC Q9UHJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Intermediate prolactin receptor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20054419; PubMed=10585417; DOI=10.1074/jbc.274.50.35461;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
RT prolactin receptor."
RL J. Biol. Chem. 274:35461-35468 (1999).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
```


RA Gould D., Djiane J., Kelly P.A.;

RT "Identification of a cDNA encoding a long form of prolactin receptor

RT in human hepatoma and breast cancer cells.";

RL Mol. Endocrinol. 3:1455-1461(1989).

RN [2]

RP NUCLEOTIDE SEQUENCE (ISOFORM 1).

RX MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;

RA Hu Z.-Z., Zhuang L., Meng J., Leonides M., Dufau M.L.;

RT "The human prolactin receptor gene structure and alternative promoter

RT utilization: the generic promoter hP111 and a novel human promoter

RT hP(N)".

RL J. Clin. Endocrinol. Metab. 84:1153-1156 (1999).

RN [3]

RP NUCLEOTIDE SEQUENCE (ISOFORM 2).

RC TISSUE=Mammary carcinoma;

RA Kline J.B., Clevenger C.V.;

RT "Characterization of a novel and functional human prolactin receptor

RT isoform (delta-S1 PRLr) containing only one extracellular fibronectin-

RT like domain.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM 1).

RC TISSUE=Placenta;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RT Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RT Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heide F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalhus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [5]

RP PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).

RC TISSUE=Mammary carcinoma;

RX MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;

RA Fuh G., Wells J.A.;

RT "Prolactin receptor antagonists that inhibit the growth of breast

RT cancer cell lines.";

RL J. Biol. Chem. 270:13133-13137 (1995).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.

RX MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;

RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;

RT "The X-ray structure of a growth hormone-prolactin receptor complex.";

RL Nature 372:478-481 (1994).

CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone

CC prolactin.

CC -!- INTERACTION:

CC P51956:NEK3; NbExp=1; IntAct=EBI-476182, EBI-476041;

CC P52735:VAV2; NbExp=1; IntAct=EBI-476182, EBI-297549;

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1;

CC IsoId=P16471-1; Sequence=Displayed;

CC Name=2; Synonyms=Delta-S1;

CC IsoId=P16471-2; Sequence=VSP_001720;

CC Name=3;

CC IsoId=P16471-3; Sequence=VSP_012620, VSP_012621;

CC Note=Soluble isoform that appears specific for the BT-474 breast

CC cancer cell line;

CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein

CC folding and thereby efficient intracellular transport and cell-

CC surface receptor binding.

CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or

CC activation.

CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 1

CC subfamily.

CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL; M31661; AAA60174.1; -; mRNA.

DR EMBL; AF091870; AAD32032.1; -; Genomic DNA.

DR EMBL; AF091863; AAD32032.1; JOINED; Genomic DNA.

DR EMBL; AF091864; AAD32032.1; JOINED; Genomic DNA.

DR EMBL; AF091865; AAD32032.1; JOINED; Genomic DNA.

DR EMBL; AF091866; AAD32032.1; JOINED; Genomic DNA.

DR EMBL; AF091867; AAD32032.1; JOINED; Genomic DNA.

DR EMBL; AF091868; AAD32032.1; JOINED; Genomic DNA.

DR EMBL; AF091869; AAK32703.1; -; mRNA.

DR EMBL; BC059392; AAH59392.1; -; mRNA.

DR EMBL; S78505; AAB34470.1; -; mRNA.

DR PIR; A40144; A40144.

DR PDB; 1BP3; X-ray; B=25-235.

DR IntAct; P16471; -.

DR ENSembl; ENSG00000113494; Homo sapiens.

DR HGNC; HGNC:9446; PRLR.

DR MIM; 176761; -.

DR GO; GO:0009986; C:cell surface; IDA.

DR GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.

DR GO; GO:0004925; F:prolactin receptor activity; NAS.

DR GO; GO:0042803; F:protein homodimerization activity; NAS.

DR GO; GO:0006916; P:anti-apoptosis; NAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NAS.

DR GO; GO:0007566; P:embryo implantation; TAS.

DR GO; GO:0007595; P:lactation; NAS.

DR GO; GO:0006694; P:steroid biosynthesis; NAS.

DR GO; GO:0042110; P:T cell activation; NAS.

DR GO; GO:0007171; P:tyrosine phosphorylation of JAK2 protein; NAS.

DR GO; GO:0042977; P:cytokine receptor protein tyrosine kin. .; IDA.

DR InterPro; IPR002996; Cytokn recept_B/G.

DR InterPro; IPR003961; FN_III

DR InterPro; IPR003828; HemtreceptL_Fl.

DR Pfam; PF00041; fn3; 2.

DR PROSITE; PS00853; FN3; 2.

DR PROSITE; PS01352; HEMATOPO REC L Fl; 1.

DR 3D-structure; Alternative splicing; Glycoprotein; Receptor; Repeat;

KW Signal; Transmembrane.

KW SIGNAL 1 24

FT CHAIN 25 622 Prolactin receptor.

FT TOPO_DOM 25 234 Extracellular (Potential).

FT TRANSMEM 235 258 Potential.

FT TOPO_DOM 259 622 Cytoplasmic (Potential).

FT DOMAIN 127 227 Fibronectin type-III 1.

FT DOMAIN 127 227 Fibronectin type-III 2.

FT MOTIF 215 219 WSXWS motif.

FT MOTIF 267 275 Box 1 motif.

FT CARBOHYD 59 59 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).

FT CARBOHYD 233 233 N-linked (GlcNAc. .) (Potential).

FT DISULFID 36 46 By similarity.

FT DISULFID 75 86 By similarity.

FT VARSPPLIC 24 124 Missing (in isoform 2).

FT VARSPPLIC 229 230 /FTId=VSP_001720.

FT VARSPPLIC 231 622 DF -> AW [in isoform 3].

FT VARSPPLIC 231 622 /FTId=VSP_012620.

FT VARSPPLIC 231 622 Missing (in isoform 3).

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:16:39 ; Search time 29.3685 Seconds
(without alignments)
1196.422 Million cell updates/sec

Title: US-09-037-657-15
Perfect score: 2317
Sequence: 1 MPAGRPVQAGARRPRRL.....NODEGILPSRRGAARGPAG 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/aaa/5 COMB.pep.*
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3: /cgn2_6/prodata/1/aaa/H'COMB.pep.*
4: /cgn2_6/prodata/1/aaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/aaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2288	98.7	425	2	US-09-071-224-6
2	2209.5	95.4	407	2	US-09-521-335-13
3	2209	95.3	405	2	US-09-012-072-2
4	2209	95.3	405	2	US-09-120-601-2
5	2176.5	93.9	422	2	US-09-866-028-32
6	2176.5	93.9	422	2	US-09-944-457-32
7	2176.5	93.9	422	2	US-09-945-584-32
8	2176.5	93.9	422	2	US-09-944-944-32
9	2176.5	93.9	422	2	US-09-945-587-32
10	2172.5	93.8	422	2	US-09-071-224-2
11	2097	90.5	385	2	US-09-071-224-19
12	2095	90.4	410	2	US-09-521-335-12
13	2094	90.4	425	2	US-09-071-224-4
14	2071.5	89.4	448	2	US-09-120-601-6
15	2051	88.5	388	2	US-09-071-224-17
16	2035	87.8	385	2	US-09-071-224-20
17	2011.5	86.8	434	2	US-09-012-072-4
18	2011.5	86.8	434	2	US-09-120-601-4
19	1978	85.4	392	2	US-09-071-224-18
20	1963	84.7	389	2	US-09-071-224-28
21	1962	84.7	389	2	US-09-071-224-22
22	1961	84.6	389	2	US-09-071-224-29
23	1960	84.6	389	2	US-09-071-224-30
24	1959	84.5	389	2	US-09-071-224-24
25	1959	84.5	389	2	US-09-071-224-25
26	1959	84.5	389	2	US-09-071-224-27
27	1958	84.5	389	2	US-09-071-224-26

28	1957	84.5	389	2	US-09-071-224-31
29	1602	69.1	303	2	US-09-071-224-23
30	1598	69.0	303	2	US-09-071-224-21
31	334	14.4	1168	2	US-09-313-942-24
32	334	14.4	1168	2	US-10-282-162-24
33	331	14.3	332	2	US-09-313-942-10
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43	329	14.2	488	2	US-08-864-564A-5
44	329	14.2	488	2	US-09-094-410-5
45	329	14.2	488	2	US-08-708-123D-5

ALIGNMENTS

RESULT 1
US-09-071-224-6
; Sequence 6, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-6

Query Match 98.7%; Score 2288; DB 2; Length 425;
Best Local Similarity 98.8%; Pred. No. 2.3e-205;
Matches 420; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPAGRGPPVAQSAARPPRLSLWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSIQ 60
DB 1 MPAGGPPAAQSAARPPRLSLWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSIH 60

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DB 61 ATCSIHGDTFGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120

QY 121 ARDGSILAGSCLYVGLPPPKPNISCSWRNMDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 121 ARDGSILAGSCLYVGLPPPKPNISCSWRNMDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 181 YQDNTCEBYHTVGPHSCHI PKDLALFTPEIWEATNRLGARSVDLTLVDVVTDP 240
DB 181 YQDNTCEBYHTVGPHSCHI PKDLALFTPEIWEATNRLGARSVDLTLVDVVTDP 240

QY 241 PPDVHVSRYGGLEDQLSVRWVPPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSCK 300
DB 241 PPDVHVSRYGGLEDQLSVRWVPPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSCK 300

QY 301 LAGLKPGETVYFVQVRCNPPGIYGSKAGIWSWSHPTAASPRSERPGGVCPRGGE 360
DB 301 LAGLKPGETVYFVQVRCNPPGIYGSKAGIWSWSHPTAASPRSERPGGVCPRGGE 360

QY 361 PSSGPVRRBKOPFLGWLKHHAYCSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGAA 420
DB 361 PSSGPVRRBKOPFLGWLKHHAYCSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGAA 420

QY 421 RGPAG 425
DB 421 RGPAG 425

RESULT 2
US-09-521-335-13
; Sequence 13, Application US/09521335
; Patent No. 6800460
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/09/521,335
; CURRENT FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-09-521-335-13

Query Match 95.4%; Score 2209.5; DB 2; Length 407;
Best Local Similarity 99.8%; Pred. No. 4.6e-198;
Matches 407; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 1 RPLSSLSWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGL 60

QY 78 YWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLP 137
DB 61 YWTLNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLP 119

QY 138 PEKPNISCSWRNMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHS 197

DB 120 PEKPNISCSWRNMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHS 179

QY 198 CHIPKDLALFTPEIWEATNRLGARSVDLTLVDVVTDPDPPDVHVSRYGGLEDQLS 257
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QY 258 VRWVSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSCLAGLKPGETVYFVQVRCN 317
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QY 318 PGIYGSKAGIWSWSHPTAASPRSERPGGVCPRGGEPSGGVRRRELKOFGLWL 377
DB 300 PGIYGSKAGIWSWSHPTAASPRSERPGGVCPRGGEPSGGVRRRELKOFGLWL 359

QY 378 KKHAYCSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGGAARGPAG 425
DB 360 KKHAYCSNLSFRLYDQWRAWMOKSHKTRNODGILPSGRGGAARGPAG 407

RESULT 3
US-09-012-072-2
; Sequence 2, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-012-072-2

Query Match 95.3%; Score 2209; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 5.1e-198;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 SSLWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGLYWT 80
DB 1 SSLWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSIQATCSIHGDTFGATAEGLYWT 60

QY 81 LNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 140
DB 61 LNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 120

QY 141 PFNISCWSRNMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHSCHI 200
DB 121 PFNISCWSRNMDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEBYHTVGPHSCHI 180

QY 201 PKDLALFTPEIWEATNRLGARSVDLTLVDVVTDPDPPDVHVSRYGGLEDQLSVRW 260
DB 181 PKDLALFTPEIWEATNRLGARSVDLTLVDVVTDPDPPDVHVSRYGGLEDQLSVRW 240

QY 261 VSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSCLAGLKPGETVYFVQVRCNPPG 320
DB 241 VSPALKDFLFOAKYQIRYRVDSVDMKVVDVSNQTSCLAGLKPGETVYFVQVRCNPPG 300

QY 321 IYGSKAGIWSWSHPTAASPRSERPGGVCPRGGEPSGGVRRRELKOFGLWLKXH 380
DB 301 IYGSKAGIWSWSHPTAASPRSERPGGVCPRGGEPSGGVRRRELKOFGLWLKXH 360

QY 381 AYCNSLSFRLYDQWRAWMOKSHKTRNODGILPSGRGGAARGPAG 425
DB 361 AYCNSLSFRLYDQWRAWMOKSHKTRNODGILPSGRGGAARGPAG 405

RESULT 4
US-09-120-601-2
; Sequence 2, Application US/09120601

Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masiaowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-120-601-2

Query Match 95.3%; Score 2209; DB 2; Length 405;
Best Local Similarity 100.0%; Pred. No. 5.1e-198;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 SSIWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTFGATAEGLYWT 80
Db 1 SSIWSPLLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLOATCSIHGDTFGATAEGLYWT 60
QY 81 INGRRLPSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 140
Db 61 INGRRLPSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSIAGSCLYVGLPPEK 120
QY 141 PNISCSNRMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEBYHTVGPHSCHI 200
Db 121 PNISCSNRMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEBYHTVGPHSCHI 180
QY 201 PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSVRVGGLEDQLSVRW 260
Db 181 PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTPPPDVHVSVRVGGLEDQLSVRW 240
QY 261 VSPPALKDFLQAKYQIRYRVEDSDVKVVDVDSNQTSCRLAGLKEGTYVYFVQVRCNPF 320
Db 241 VSPPALKDFLQAKYQIRYRVEDSDVKVVDVDSNQTSCRLAGLKEGTYVYFVQVRCNPF 300
QY 321 IYGSKKAGIWSWSHPTAASPRSERPPGGGVCPEPRGSGSPVRRBLKDFLQAKY 380
Db 301 IYGSKKAGIWSWSHPTAASPRSERPPGGGVCPEPRGSGSPVRRBLKDFLQAKY 360
QY 381 AYCSNLSFRLYDQRAWMOKSHKTRNQDREGILPSGRGAARGPAG 425
Db 361 AYCSNLSFRLYDQRAWMOKSHKTRNQDREGILPSGRGAARGPAG 405

RESULT 5
US-09-866-028-32
; Sequence 32, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-32

Query Match 93.9%; Score 2176.5; DB 2; Length 422;
Best Local Similarity 94.8%; Pred. No. 6e-195;
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;
QY 1 MPAGRPGPVAQSAARRPPRLSLWSPLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLLQ 60
Db 1 MPAGRPGPVAQSAARRPPRLSLWSPLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLLQ 57
QY 61 ATCSIHGDTFGATAEGLYWTINGRRLPSELSRLNTSTLALANLNGSRQSGDNLVCH 120
Db 58 ATCSVHGDPPGATAEGLYWTINGRRLPSELSRLNTSTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRMKDLTCRWTPGAHGETFLHTNYSKYLKRW 180
Db 118 ARDGSILAGSCLYVGLPPEKPNISCSNRMKDLTCRWTPGAHGETFLHTNYSKYLKRW 177
QY 181 YQDQDNTCEBYHTVGPHSCHI PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTP 240
Db 178 YQDQDNTCEBYHTVGPHSCHI PKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTP 237
QY 241 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSDVKVVDVDSNQTSCR 300
Db 238 PPDVHVSVRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSDVKVVDVDSNQTSCR 297
QY 301 LAGLKEGTYVYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSERPPGGGVCPEPRGGE 360
Db 298 LAGLKEGTYVYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSERPPGGGVCPEPRGGE 357
QY 361 PSSGVPVRELKDFLQAKYQIRYRVEDSDVKVVDVDSNQTSCR 420
Db 358 PSSGVPVRELKDFLQAKYQIRYRVEDSDVKVVDVDSNQTSCR 417
QY 421 RGPA 424
Db 418 RGPA 421

RESULT 6
US-09-944-457-32
; Sequence 32, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,457

Page 4

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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-32

Query Match 93.9%; Score 2176.5; DB 2; Length 422;
Best Local Similarity 94.8%; Pred. No. 6e-195;
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRPGPVAQSARRPRPLSSLLWSPLLCVLGVPRGGGAHTAVISPODPTLLIGSSLQ 60
   |||||
Db 1 MPAGRGPAAQSARRPP-PLPL--L-LLCVLGAPRAGSGAHTAVISPODPTLLIGSSL 57
   |||||

QY 61 ATCSIHGDPGATAEGLYWTNGRRLPSELSSLNTSTLALANLNGSRQSGDNLVCH 120
   |||||
Db 58 ATCSVHGDPGATAEGLYWTNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117
   |||||

QY 121 ARDGSILAGSCLVGLPPPEKPFNISCWRNMKDLTCRWTPGAHGETFLHTNYSUKYKLRW 180
   |||||
Db 118 ARDGSILAGSCLVGLPPPEKPFNVNISCWNMKDLTCRWTPGAHGETFLHTNYSUKYKLRW 177
   |||||

QY 181 YGQDNTCEEYHTVGPHSCHIPKDALFTPYEIVWEATNRLGARSVDLTLDVLDVVTDP 240
   |||||
Db 178 YGQDNTCEEYHTVGPHSCHIPKDALFTPYEIVWEATNRLGARSVDLTLDVLDVVTDP 237
   |||||

QY 241 PPDVHVSVRGLEDQLSVRWVSPALKDPLFOAKYQIRYRVESVDWKVDDVSNQTSR 300
   |||||
Db 238 PPDVHVSVRGLEDQLSVRWVSPALKDPLFOAKYQIRYRVESVDWKVDDVSNQTSR 297
   |||||

QY 301 LAGLKPTGYVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGVCPEPRGGE 360
   |||||
Db 298 LAGLKPTGYVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGVCPEPRGGE 357
   |||||

QY 361 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQRAWWQKSHKTRNDEGILPSRRGAA 420
   |||||
Db 358 PSSGPVRELLKQFLGWLKKHAYCSNLSFRLYDQRAWWQKSHKTRNDEGILPSRRGTA 417
   |||||

QY 421 RGA 424
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Db 418 RGA 421

RESULT 7
US-09-945-584-32
; Sequence 32, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584

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; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 06/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000

;
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-945-584-32

Query Match 93.9%; Score 2176.5; DB 2; Length 422;
Best Local Similarity 94.8%; Pred. No. 6e-195;
Matches 402; Conservative 5; Mismatches 14; Indels 3; Gaps 2;

QY 1 MPAGRGPVAAQARPPRLPSLSWPLLCVIGVPRGSGAHTAVISPDPTLLIGSSLLQ 60
Db 1 MPAGRGPVAAQARPPRLPSLSWPLLCVIGVPRGSGAHTAVISPDPTLLIGSSLL 57

QY 61 ATCSIHGDTPGATAEGLYWTNGRRLLPSLSRLNTSTLALANLNGSRQSGDNLVCH 120
Db 58 ATCSVHGDPGATAEGLYWTNGRRLLPPELSRVNASTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLYVGLPPEKPNISCSNRMKDLTCRWTPGAHGETFLHTNYSLKYLRLW 180
Db 118 ARDGSILAGSCLYVGLPPEKPNISCSNRMKDLTCRWTPGAHGETFLHTNYSLKYLRLW 177

QY 181 YGQDNTCEYHTVGHSHCHIPKDLALFTPYEIVWEATNRLGARSQVLTLDVVTDDP 240
Db 178 YGQDNTCEYHTVGHSHCHIPKDLALFTPYEIVWEATNRLGARSQVLTLDVVTDDP 237

QY 241 PPDVHVS RVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVWKVVDDVSNQTSR 300
Db 238 PPDVHVS RVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVWKVVDDVSNQTSR 297

QY 301 LAGLKP GTVYFVQVRCNPPGIYGSKKAGIWSWSHPTAASTPRSERPPGGVCEPRGGE 360
Db 298 LAGLKP GTVYFVQVRCNPPGIYGSKKAGIWSWSHPTAASTPRSERPPGGVCEPRGGE 357

QY 361 PSSGVPVRELKQFLGWLKKHAYCSNLSFRLYQDRAWMQSHKTRNQDGLPSGRGAA 420
Db 358 PSSGVPVRELKQFLGWLKKHAYCSNLSFRLYQDRAWMQSHKTRNQDGLPSGRGTA 417

QY 421 RGPA 424
Db 418 RGPA 421

RESULT 8
US-09-944-944-32
; Sequence 32, Application US/09944944
; Patent No. 6929947
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Batton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548FIC1
; CURRENT APPLICATION NUMBER: US/09/944,944

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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-32

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Query Match	93.9%	Score 2176.5	DB 2	Length 422
Best Local Similarity	94.8%	Pred. No. 66-195		
Matches 402	Conservative 5	Mismatches 14	Indels 3	Gaps 2
Qy 1	MPAGRPEVQAQSARRPRPISLSSWSPILLVLGVPRGGSGAHTAVISPDQPTLLIGSSLIQ 60			
Db 1	MPAGRRGPAAQSAARRPP-PLLPLL--LALLCVLGAPRAGSGAHTAVISPDQPTLLIGSSLL 57			
Qy 61	ATCSIHGDTGATAGELYWTINGRRLLPSELRRLLNTSTLALANLNGSRQSGDNLVCH 120			
Db 58	ATCSVHGDDPGCATAGELYWTINGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCH 117			
Qy 121	ARDGSIILAGSCLLYGLPEKPPFNISCSWRNNKDLTCRWTPGAHGTFTHNTYSLKYKLRW 180			
Db 118	ARDGSIILAGSCLLYGLPEKPPVNTSCWKNMKDLTCRWTPGAHGTFTHNTYSLKYKLRW 177			
Qy 181	YGQDNTCEEYHTVGPHSCHIPKOLALFTPYEIIWEATNRLGSARSDVLTLDVLDVVTDP 240			
Db 178	YGQDNTCEEYHTVGPHSCHIPKOLALFTPYEIIWEATNRLGSARSDVLTLDILDVVTDP 237			
Qy 241	PPDVHSRVUGLEDQLSVRWVSPPALXDFLPQAKYQIRYRVEDSDVKWVDDVDSNOTSCR 300			
Db 238	PPDVHSRVUGLEDQLSVRWVSPPALXDFLPQAKYQIRYRVEDSDVKWVDDVDSNOTSCR 297			
Qy 301	LAGLKPQTVYFVQVRCNPPFGYIGSKKAGIWEWSHPTAASTPRSERPOGGGVCPRGGE 360			
Db 298	LAGLKPQTVYFVQVRCNPPFGYIGSKKAGIWEWSHPTAASTPRSERPOGGGACPRGGE 357			
Qy 361	PSSGPVRRLELKQFLGWLKKHAYCSNLGFRLLDQWRAMWQKSHKTNQDEGILLPSGRRGAA 420			
Db 358	PSSGPVRRLELKQFLGWLKKHAYCSNLGFRLLDQWRAMWQKSHKTNQDEGILLPSGRRGTA 417			
Qy 421	RGPA 424			
Db 418	RGPA 421			

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RESULT 10
US-09-071-224-2
; Sequence 2, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSEQ for Windows Version 2.0									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/09/071,224									
; FILING DATE:									
; CLASSIFICATION:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER:									
; FILING DATE:									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Lunn, Paul G									
; REGISTRATION NUMBER: 32,743									
; REFERENCE/DOCKET NUMBER: 96-22									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: 206-442-6627									
; TELEFAX: 206-442-6678									
; TELEX:									
; INFORMATION FOR SEQ ID NO: 2:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 422 amino acids									
; TYPE: amino acid									
; STRANDEDNESS: single									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
; FRAGMENT TYPE: internal									
US-09-071-224-2									
Query Match 93.8%; Score 2172.5; DB 2; Length 422;									
Best Local Similarity 94.6%; Pred. No. 1.4e-194;									
Matches 401; Conservative 6; Mismatches 14; Indels 3; Gaps 2;									
Qy	1	MPAGRGVQAQARRPRRLSSLLVLCVLPGRGSGAHTAVISPODPTLLIGSSLQ	60						
Db	1	MPAGRRGPAQASARPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL	57						
Qy	61	ATCSIHGDPGATAEGLYWTNGRRLPSELRLNTSTLALANLNGSRQSGDNLVCH	120						
Db	58	ATCSVHGDPGATAEGLYWTNGRRLPPELSRVINASTLALANLNGSRQSGDNLVCH	117						
Qy	121	ARDGSLAGSCLVGLPPEKPFNISCSWRNMKDLTCRWTPGAHGETFLHTNYSLKYLKW	180						
Db	118	ARDGSLAGSCLVGLPPEKPFNISCSWKMKDLTCRWTPGAHGETFLHTNYSLKYLKW	177						
Qy	181	YGQDNTCEEVHTVGPHSCHIPKDIALFTPYEIVWEATNRLGARSVDLTLVDLVVTTDP	240						
Db	178	YGQDNTCEEVHTVGPHSCHIPKDIALFTPYEIVWEATNRLGARSVDLTLVDLVVTTDP	237						
Qy	241	PPDVHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDKVVDVSNQTSR	300						
Db	238	PPEVHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDKVVDVSNQTSR	297						
Qy	301	LAGLKPGTVYFVQVRCNPFGIYSGKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGE	360						
Db	298	LAGLKPGTVYFVQVRCNPFGIYSGKKAGIWESEWHPHTAASTPRSERPGGGVCEPRGGE	357						
Qy	361	PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMQSHKTRNQDEGILPSGRGAA	420						
Db	358	PSSGPRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMQSHKTRNQDEGILPSGRGTA	417						
Qy	421	RGPA 424							
Db	418	RGPA 421							
RESULT 11									
US-09-071-224-19									
; Sequence 19, Application US/09071224									
; Patent No. 6271343									
; GENERAL INFORMATION:									
; APPLICANT: Lok, Si									
; APPLICANT: Preenell, Scott R.									
; APPLICANT: Jelmeberg, Anna C.									
; APPLICANT: Gilbert, Teresa									
; APPLICANT: Foster, Donald C.									
; APPLICANT: Adams, Robyn L.									
; APPLICANT: Lehner, Joyce M.									
; TITLE OF INVENTION: MAMMALIAN ZCYTORS									
; NUMBER OF SEQUENCES: 37									
; FILING DATE:									
; CLASSIFICATION:									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER:									
; FILING DATE:									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Lunn, Paul G									
; REGISTRATION NUMBER: 32,743									
; REFERENCE/DOCKET NUMBER: 96-22									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: 206-442-6627									
; TELEFAX: 206-442-6678									
; TELEX:									
; INFORMATION FOR SEQ ID NO: 2:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 422 amino acids									
; TYPE: amino acid									
; STRANDEDNESS: single									
; TOPOLOGY: linear									
; MOLECULE TYPE: protein									
; FRAGMENT TYPE: internal									
US-09-071-224-19									
Query Match 90.5%; Score 2097; DB 2; Length 385;									
Best Local Similarity 99.7%; Pred. No. 1.4e-187;									
Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	41	AHTAVISPODPTLLIGSSLQATCSIHGDPGATAEGLYWTNGRRLPSELRLNTSTLA	100						
Db	1	AHTAVISPODPTLLIGSSLHATCSIHGDPGATAEGLYWTNGRRLPSELRLNTSTLA	60						
Qy	101	LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPFNISCSWRNMKDLTCRWTP	160						
Db	61	LALANLNGSRQSGDNLVCHARDGSLAGSCLVGLPPEKPFNISCSWRNMKDLTCRWTP	120						
Qy	161	GAHGETFLHTNYSLKYLKWYQDNTCEEVHTVGPHSCHIPKDIALFTPYEIVWEATNRL	220						
Db	121	GAHGETFLHTNYSLKYLKWYQDNTCEEVHTVGPHSCHIPKDIALFTPYEIVWEATNRL	180						
Qy	221	GSARSVDLTLVDLVVTTDPPDVHVS RVGGLDQLSVRWVSPALKDFLFOAKYQIRYR	280						
Db	181	GSARSVDLTLVDLVVTTDPPDVHVS RVGGLDQLSVRWVSPALKDFLFOAKYQIRYR	240						
Qy	281	VEDSDVKVVDVSNQTSCLAGLKPGTVYFVQVRCNPFGIYSGKKAGIWESEWHPHTAA	340						
Db	241	VEDSDVKVVDVSNQTSCLAGLKPGTVYFVQVRCNPFGIYSGKKAGIWESEWHPHTAA	300						
Qy	341	TPRSERPGGGVCEPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMQ	400						
Db	301	TPRSERPGGGVCEPRGGEPSGPPVRRRELKQFLGWLKKHAYCSNLSFRLYDQRAWMQ	360						
Qy	401	SHKTRNQDEGILPSGRGGAARGPAG 425							
Db	361	SHKTRNQDEGILPSGRGGAARGPAG 385							

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RESULT 12
US-09-521-335-12
; Sequence 12, Application US/09521335
; Patent No. 6800460
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/09/521,335
; CURRENT FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 410
; TYPE: PRT
; ORGANISM: primate
US-09-521-335-12

Query Match          90.4%; Score 2095; DB 2; Length 410;
Best Local Similarity 93.9%; Pred. No. 2.4e-187;
Matches 388; Conservative 6; Mismatches 13; Indels 6; Gaps 3;

QY 1 MPAGRPGVPAQSARPPRLPSLWSPLLCVLGVRPGSGAHTAVISPODPTLLIGSSILQ 60
DB 1 MPAGRPGVPAQSARPP-PLPLPL-LLLVLGAPRAGSGAHTAVISPODPTLLIGSSIL 57

QY 61 ATCSIHGDTPGTAGELVTLNRRLLPSLSLLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDPGPGTAGELVTLNRRLLPSLSLLNTSTLALANLNGSRQSGDNLVCH 117

QY 121 ARDGSILAGSCLVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 118 ARDGSILAGSCLVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177

QY 181 YQDNTCEYHTVGPCHSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTDP 240
DB 178 YQDNTCEYHTVGPCHSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTDP 237

QY 241 PPDVHVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300
DB 238 PPDVHVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 297

QY 301 LAGLKGTVYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360
DB 298 LAGLKGTVYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 357

QY 361 PSSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQ 413
DB 358 PSSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQ---VLP 407

RESULT 13
US-09-071-224-4
; Sequence 4, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
```

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; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-4

Query Match          90.4%; Score 2094; DB 2; Length 425;
Best Local Similarity 94.8%; Pred. No. 3.1e-187;
Matches 386; Conservative 5; Mismatches 12; Indels 4; Gaps 2;

QY 1 MPAGRPGVPAQSARPPRLPSLWSPLLCVLGVRPGSGAHTAVISPODPTLLIGSSILQ 60
DB 1 MPAGRPGVPAQSARPP-PLPLPL-LLLVLGAPRAGSGAHTAVISPODPTLLIGSSIL 56

QY 61 ATCSIHGDTPGTAGELVTLNRRLLPSLSLLNTSTLALANLNGSRQSGDNLVCH 120
DB 57 ATCSVHGDPGPGTAGELVTLNRRLLPSLSLLNTSTLALANLNGSRQSGDNLVCH 116

QY 121 ARDGSILAGSCLVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
DB 117 ARDGSILAGSCLVGLPPEKPNISCSWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 176

QY 181 YQDNTCEYHTVGPCHSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTDP 240
DB 177 YQDNTCEYHTVGPCHSCHIPKDLALFTPEYIWEATNRLGARSVDLTLDVLDVVTTDP 236

QY 241 PPDVHVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 300
DB 237 PPDVHVSRRVGGLEDQLSVRWVSPALPKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSR 296

QY 301 LAGLKGTVYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 360
DB 297 LAGLKGTVYFVQVRCNPFYIYGSKKAGIWSWSHPTAASPRSRPFGGVCPRGGE 356

QY 361 PSSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQ 407
DB 357 PSSGPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQ 403

RESULT 14
US-09-120-601-6
; Sequence 6, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
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; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 448
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-6

Query Match      89.4%; Score 2071.5; DB 2; Length 448;
Best Local Similarity 90.0%; Pred. No. 4.3e-185;
Matches 386; Conservative 5; Mismatches 13; Indels 25; Gaps 3;

QY 1 MPAGRPGPVAQARPPRLSSILWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSIIQ 60
DB 1 MPAGRGPAQAQARPP-PLLPL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSII 57
QY 61 ATCSIHGDPGATAEGLYWTNGRLPSELRLNTSTLALANLNGSRQSGDNLVCH 120
DB 58 ATCSVHGDPGATAEGLYWTNGRLPSELRLNASTLALANLNGSRQSGDNLVCH 117
QY 121 ARDGSILAGSCLVGLPPEKPNISCSWNRNMKDLTCRWTPGAHGETFLHTNYSCLKYLRW 180
DB 118 ARDGSILAGSCLVGLPPEKPNISCSWNRNMKDLTCRWTPGAHGETFLHTNYSCLKYLRW 177
QY 181 YGQDNTCEHYHTVGPHSCHIPKDLALFTPEYIWEATNRLGSARSDVLTLDVID----- 234
DB 178 YGQDNTCEHYHTVGPHSCHIPKDLALFTPEYIWEATNRLGSARSDVLTLDIDVGSHP 237
QY 235 -----VTTDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQIR 278
DB 238 LPSPATPGLSLLVRGKVVTTDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQIR 297
QY 279 YRVEDSDVMKWVDDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPTA 338
DB 298 YRVEDSDVMKWVDDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPTA 357
QY 339 ASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWM 398
DB 358 ASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWM 417
QY 399 QKSHKTRNQ 407
DB 418 QKSHKTRNQ 426

RESULT 15
US-09-071-224-17
; Sequence 17, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTOR5
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-224-17

Query Match      88.5%; Score 2051; DB 2; Length 388;
Best Local Similarity 96.4%; Pred. No. 2.9e-183;
Matches 373; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 38 GSGAHTAVISPODPTLLIGSSIIQATCSIHGDPGATAEGLYWTNGRLPSELRLNTS 97
DB 1 GSGAHTAVISPODPTLLIGSSIIATCSVHGDPGATAEGLYWTNGRLPSELRLNAS 60
QY 98 TLALANLNGSRQSGDNLVCHARDGSTILAGSCLVGLPPEKPNISCSWNRNMKDLTCR 157
DB 61 TLALANLNGSRQSGDNLVCHARDGSTILAGSCLVGLPPEKPNISCSWNRNMKDLTCR 120
QY 158 WTPGAHGETFLHTNYSCLKYLRWYQDNTCEHYHTVGPHSCHIPKDLALFTPEYIWEAT 217
DB 121 WTPGAHGETFLHTNYSCLKYLRWYQDNTCEHYHTVGPHSCHIPKDLALFTPEYIWEAT 180
QY 218 NRLGSARSDVLTLDVIDVVTDDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQI 277
DB 181 NRLGSARSDVLTLDIDVVTDDPPDVHVSVRVGLEDQLSVRWVSPPALKDFLFOAKYQI 240
QY 278 YRVEDSDVMKWVDDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPT 337
DB 241 YRVEDSDVMKWVDDVSNQTSCLAGLKPGTVYFVQVRCNPGFYGSKKAGIWEWSHPT 300
QY 338 AASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 397
DB 301 AASTPRSERPGGGVCEPRGGEPSSGPVRRRELKQFLGWLKKHAYCSNLSFRLYDQWRAW 360
QY 398 MOKSHKTRNQDEGILPSGRGARGPA 424
DB 361 MOKSHKTRNQDEGILPSGRGARGPA 387

Search completed: April 11, 2006, 02:18:58
Job time : 30.3685 secs
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Result No.	Score	Query			DB	ID	Description
		Match	Length	\$			
1	2290	100.0	421	4	AAE00826	Aae00826 Murine ha	
2	2279.5	99.5	421	2	AAE05782	Aay05782 Human typ	
3	2279.5	99.5	422	2	AAE06479	Aay06479 Human tum	
4	2279.5	99.5	422	2	AAE17825	Aay17825 Human PRO	
5	2279.5	99.5	422	2	AAE26339	Aay26339 Human U4	
6	2279.5	99.5	422	3	AAE01316	Aab01316 Human PRO	
7	2279.5	99.5	422	3	AAE93686	Aay93686 Amino aci	
8	2279.5	99.5	422	4	AAE63545	Aae63545 Amino aci	
9	2279.5	99.5	422	6	ABU55925	Abu55925 Human sec	
10	2279.5	99.5	422	6	ABU60235	Abu60235 Human PRO	
11	2279.5	99.5	422	6	ABG72776	Abg72776 Human cyt	
12	2279.5	99.5	422	6	ABU64921	Abu64921 Human sec	
13	2279.5	99.5	422	6	ABU58355	Abu58355 Novel hum	
14	2279.5	99.5	422	6	ABU57241	Abu57241 Human PRO	
15	2279.5	99.5	422	6	ABU56306	Abu56306 Human sec	
16	2279.5	99.5	422	6	ABU60346	Abu60346 Novel hum	
17	2279.5	99.5	422	6	ABU11307	Abu11307 Human pro	
18	2279.5	99.5	422	6	ABU67126	Abu67126 Human PRO	
19	2279.5	99.5	422	7	ADC25788	Adc25788 Human sec	
20	2279.5	99.5	422	7	ADC25546	Adc25546 Human sec	
21	2279.5	99.5	422	7	ADC25667	Adc25667 Human sec	
22	2279.5	99.5	422	7	ADH27452	Adh27452 Human sec	
23	2279.5	99.5	422	8	ADH71501	Adh71501 Human sec	
24	2279.5	99.5	422	8	ADG63444	Adg63444 Human sec	

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CC haemopoietin receptor, NR6 protein, encoded by NR6 DNA
CC Revised record issued on 09-SEP-2004 : Correction to Organism field
XX SQ Sequence 421 AA;
Query Match 100.0%; Score 2290; DB 4; Length 421;
Best Local Similarity 100.0%; Pred. No. 5.1e-185; Indels 0; Gaps 0;
Matches 421; Conservative 0; Mismatches 0;
QY 1 MPAGRRGPAQAQARRPPPLPILLLLCVLGAPRAGSGAHTAVISPDQPTLLIGSSLLATCS 60
DB 1 MPAGRRGPAQAQARRPPPLPILLLLCVLGAPRAGSGAHTAVISPDQPTLLIGSSLLATCS 60
QY 61 VHGDDPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120
DB 61 VHGDDPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120
QY 121 SILAGSCLVGLPPEKPNVISCWSKNMKDLCRWTPGAHGETFLHTNYSKYLKRWYQD 180
DB 121 SILAGSCLVGLPPEKPNVISCWSKNMKDLCRWTPGAHGETFLHTNYSKYLKRWYQD 180
QY 181 NTCEBYHTVGPCHSCHKDLCALFTTPEIWEATNRLGARSVDLTLDLDVVTTPPPDV 240
DB 181 NTCEBYHTVGPCHSCHKDLCALFTTPEIWEATNRLGARSVDLTLDLDVVTTPPPDV 240
QY 241 HVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRVRVEDSVDWKVVDVSNQTSRLAGL 300
DB 241 HVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRVRVEDSVDWKVVDVSNQTSRLAGL 300
QY 301 KPGTVYFVQVRCNPFGIYGSKKAGIWESEWSPHTAATPSERPGGACPRGGEPSG 360
DB 301 KPGTVYFVQVRCNPFGIYGSKKAGIWESEWSPHTAATPSERPGGACPRGGEPSG 360
QY 361 PVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGPA 420
DB 361 PVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGPA 420
QY 421 R 421
DB 421 R 421
RESULT 2
ID AAY05782
XX AAY05782 standard; protein; 422 AA.
AC AAY05782;
XX 02-AUG-1999 (first entry)
DE Human type 1 cytokine receptor GBRI-ILR.
XX GBRI-ILR; hGBR-ILR, cytokine receptor; human; cancer; obesity;
KW inflammation; septic shock; AIDS; embryo development; lung infection;
KW cytostatic; anorectic; immunosuppressive; antibacterial; antiviral;
KW antiinflammatory; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..37
FT /note= "signal peptide"
FT Protein 38..422
FT /note= "mature protein; a polypeptide comprising amino
FT acids 38-422 is also claimed in Claim 1a"
XX
XX WO920755-A2.
XX
XX 29-APR-1999.
XX
XX 14-OCT-1998; 98WO-EP006497.
XX
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PR 16-OCT-1997; 97GB-00021961.
XX (GLAX ) GLAXO GROUP LTD.
PA Elson G, Gauchat J, Kosco-Vilbois M;
XX WPI; 1999-288305/24.
XX N-PSDB; AAX25489.
PT Novel human or mouse type I cytokine receptors hGBRI-ILR or mGBRI-ILR,
FT useful for treating e.g. cancer, immune disorders, obesity and AIDS.
PS Claim 1a; Fig 4; 41pp; English.
XX
CC The present sequence represents a novel type 1 cytokine receptor that has
CC been termed human GBRI-ILR as it is believed to be an interleukin
CC receptor, or at least a substantial part of such a receptor. The sequence
CC is predicted from an isolated full-length cDNA clone (see AAX25489)
CC obtained from a human placental cDNA library. GBRI-ILR mRNA is expressed
CC most strongly in spleen, thymus, lymph node, appendix, bone marrow,
CC thymoid, adrenal cortex, stomach, heart, placenta and skeletal muscle,
CC suggesting a role for GBRI-ILR in the immune system. In human foetal
CC tissue, strong expression is seen in the lung, but not in brain, kidney
CC or liver. A GBRI-ILR receptor has also been identified in mice (see
CC AAY05783). The high degree of conservation of amino acids between the
CC human and murine polypeptides indicates that this receptor is
CC functionally important. GBRI-ILR polypeptides, nucleic acids, antibodies,
CC agonists and antagonists can be used to treat e.g. cancer, immune
CC disorders, obesity (in view of homology to the leptin receptor),
CC embryonic developmental disorders, AIDS, septic shock and lung infection
CC (claimed)
XX Sequence 422 AA;
SQ
Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAQARRPPPLP-LILLLCVLGAPRAGSGAHTAVISPDQPTLLIGSSLLATC 59
DB 1 MPAGRRGPAQAQARRPPPLP-LILLLCVLGAPRAGSGAHTAVISPDQPTLLIGSSLLATC 60
QY 60 SVHGDDPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
DB 61 SVHGDDPGATAGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSILAGSCLVGLPPEKPNVISCWSKNMKDLCRWTPGAHGETFLHTNYSKYLKRWYQ 179
DB 121 GSILAGSCLVGLPPEKPNVISCWSKNMKDLCRWTPGAHGETFLHTNYSKYLKRWYQ 180
QY 180 DNTCEBYHTVGPCHSCHKDLCALFTTPEIWEATNRLGARSVDLTLDLDVVTTPPPD 239
DB 181 DNTCEBYHTVGPCHSCHKDLCALFTTPEIWEATNRLGARSVDLTLDLDVVTTPPPD 240
QY 240 VHSVRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRVRVEDSVDWKVVDVSNQTSRLAG 299
DB 241 VHSVRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRVRVEDSVDWKVVDVSNQTSRLAG 300
QY 300 LKPGTVYFVQVRCNPFGIYGSKKAGIWESEWSPHTAATPSERPGGACPRGGEPS 359
DB 301 LKPGTVYFVQVRCNPFGIYGSKKAGIWESEWSPHTAATPSERPGGACPRGGEPS 360
QY 360 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGP 419
DB 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGP 420
QY 420 AR 421
DB 421 AR 422
RESULT 3
AAY06479
```

ID AAY06479 standard; protein; 422 AA.
 AC AAY06479;
 DT 27-SEP-1999 (first entry)
 XX Human tumour-associated protein PRO327.
 DE PRO327; UNQ288; cancer; tumour; diagnosis; therapy; human.
 KW Homo sapiens.
 OS Homo sapiens.
 XX WO9935170-A2.
 PN 15-JUL-1999.
 PD 05-JAN-1999; 99WO-US000106.
 PF 05-JAN-1998; 98US-0070440P.
 PR 29-APR-1998; 98US-0083500P.
 XX 22-MAY-1998; 98US-0086414P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 20-NOV-1998; 98US-0109304P.
 XX (GETH) GENENTECH INC.
 PA Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;
 PI Wood WI;
 XX WPI; 1999-430385/36.
 DR N-PSDB; AAX87256.
 XX Antibody against proteins expressed in neoplastic cells, useful for tumor
 PT diagnosis and treatment.
 XX Example 1; Fig 6; 162pp; English.
 XX This sequence represents human PRO327 (UNQ288), a 46.3 kDa protein (pI
 CC 9.42) encoded by the novel cDNA clone DNA38113 (see AAX87256).
 CC Amplification of DNA38113 occurs in various lung and colon tumours and
 CC cell lines, suggesting a significant role in tumour formation and growth.
 CC Antagonists (e.g. antibodies) directed against PRO327 are expected to
 CC have utility in cancer therapy. The invention identifies 14 genes (see
 CC AAX87254-67) that are amplified in the genome of tumour cells. Such
 CC amplification is expected to be associated with overexpression of the
 CC gene product and to contribute to tumorigenesis. The encoded proteins
 CC (see AAY06477-90) may be useful targets for the diagnosis and/or
 CC treatment (including prevention) of certain cancers, and may act as
 CC predictors of the prognosis of tumour treatment. Antibodies that bind the
 CC proteins are claimed and used in claimed cancer diagnostic kits
 XX Sequence 422 AA;
 SQ

Query Match 99.5%; Score 2279.5; DB 2; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3.9e-184;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAARRPPLP-LLLCVLGAPRAGAGTAATVISPQDPTLLIGSSLLATC 59
 DB 1 MPAGRRGPAQAARRPPLP-LLLCVLGAPRAGAGTAATVISPQDPTLLIGSSLLATC 60
 QY 60 SVHGDPGATAGLYWTNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 119
 DB 61 SVHGDPGATAGLYWTNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 120
 QY 120 GSILAGSLYVGLPPEKPNVISCWKNMDLTCRWTPGAHGETFLHTNYSLKYLRYGQ 179
 DB 121 GSILAGSLYVGLPPEKPNVISCWKNMDLTCRWTPGAHGETFLHTNYSLKYLRYGQ 180
 QY 180 DNTCEHYHTVGHSCHPKDLALFTPEIWEATNRLGARSVDLTLIDVVTTDPPPD 239
 DB 181 DNTCEHYHTVGHSCHPKDLALFTPEIWEATNRLGARSVDLTLIDVVTTDPPPD 240

QY 240 VHVSRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 299
 XX |||||
 DB 241 VHVSRVGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 300
 XX |||||
 QY 300 LKPGTVYFVQVRCNPFYIYGSKKAGIWSKSHPTAASTPRSRPFGGCGACPRGGPSS 359
 XX |||||
 DB 301 LKPGTVYFVQVRCNPFYIYGSKKAGIWSKSHPTAASTPRSRPFGGCGACPRGGPSS 360
 XX |||||
 QY 360 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQDSGILPSGRRGTARGP 419
 XX |||||
 DB 361 GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNQDSGILPSGRRGTARGP 420
 XX |||||
 QY 420 AR 421
 DB 421 AR 422
 XX |||||
 RESULT 4
 AAY17825
 ID AAY17825 standard; protein; 422 AA.
 XX AAY17825;
 AC AAY17825;
 XX 12-AUG-1999 (first entry)
 DT Human PRO327 protein sequence.
 XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 KW secreted protein; transmembrane protein; inflammation disorder.
 XX Homo sapiens.
 OS WO9928462-A2.
 PN 10-JUN-1999.
 PD 01-DEC-1998; 98WO-US025108.
 PF 03-DEC-1997; 97US-0067411P.
 PR 11-DEC-1997; 97US-0069278P.
 PR 11-DEC-1997; 97US-0069334P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 16-DEC-1997; 97US-0069696P.
 PR 16-DEC-1997; 97US-0069702P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 18-DEC-1997; 97US-0069873P.
 PR 05-JAN-1998; 98US-0070440P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-FEB-1998; 98US-0075945P.
 XX (GETH) GENENTECH INC.
 PA Wood WI, Goddard A, Gurney AL, Yuan J, Baker KP, Chen J;
 XX WPI; 1999-371118/31.
 DR N-PSDB; AAX80050.
 XX Nucleic acids encoding PRO secreted and transmembrane proteins.
 PT Claim 12; Fig 17; 123pp; English.
 XX The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes and
 CC primers. They can be used in a range of diseases related to proteins that
 CC they have homology with, e.g. a PRO protein having homology to complement

FT Modified-site /note= "N-myristoylation site"
FT 44..48
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 73..79
FT /note= "N-myristoylation site"
FT Modified-site 79..83
FT /note= "amidation site"
FT Modified-site 92..96
FT /note= "N-glycosylation site"
FT Modified-site 104..108
FT /note= "N-glycosylation site"
FT Modified-site 121..127
FT /note= "N-myristoylation site"
FT Modified-site 140..144
FT /note= "N-glycosylation site"
FT Modified-site 168..172
FT /note= "N-glycosylation site"
FT Modified-site 179..185
FT /note= "N-myristoylation site"
FT Modified-site 183..187
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 205..209
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 218..224
FT /note= "N-myristoylation site"
FT Modified-site 292..296
FT /note= "N-glycosylation site"
FT Modified-site 300..306
FT /note= "N-myristoylation site"
FT Modified-site 317..323
FT /note= "N-myristoylation site"
FT Modified-site 320..326
FT /note= "N-myristoylation site"
FT Modified-site 325..332
FT /note= "Growth factor and cytokines receptor family signature 2"
FT Modified-site 347..353
FT /note= "N-myristoylation site"
FT Modified-site 355..361
FT /note= "N-myristoylation site"
FT Modified-site 382..386
FT /note= "N-glycosylation site"
FT Modified-site 407..413
FT /note= "N-myristoylation site"
FT Modified-site 411..415
FT /note= "amidation site"
FT Modified-site 413..417
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"
FT
FT
XX WO200037640-A2.
PN
XX
XX
XX 29-JUN-2000.
XX
XX 16-DEC-1999; 99WO-US030095.
XX
XX 22-DEC-1998; 98US-0113296P.
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028565.
XX (GETH) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
XX Wood WI;
XX WPI; 2000-452188/39.
XX
XX N-PSDB; AAA46902.

XX New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation.
XX
XX Claim 61; Fig 6; 220pp; English.
XX
XX The present sequence represents a novel human polypeptide. The
CC specification describes novel polypeptides designated PRO201, PRO292,
CC PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017,
CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the
CC genome of tumour cells. The polypeptides are believed to contribute to
CC tumorigenesis. The polypeptides are useful target for the identification
CC of certain cancers, and may act as predictors of the prognosis of tumour
CC treatment. Antibodies against these polypeptides are useful in the
CC treatment and diagnosis of neoplastic cell growth and proliferation in
CC mammals
XX
XX Sequence 422 AA;
SQ
Query Match 99.5%; Score 2279.5; DB 3; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAQARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59
DB 1 MPAGRRGPAQAQARRPPPLLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
QY 60 SVHGDPGATAGLYWTTLNGRRRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 119
DB 61 SVHGDPGATAGLYWTTLNGRRRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPNVSCWSKNMKDLTCRWTPGAHGTFLHTNYSLKYKLRWYQ 179
DB 121 GSILAGSCLYVGLPPEKPNVSCWSKNMKDLTCRWTPGAHGTFLHTNYSLKYKLRWYQ 180
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDLVDVTTDDPPD 239
DB 181 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDLVDVTTDDPPD 240
QY 240 VHVSRVGGLEDQLSVRVWSPPALKDFLQAKYQIRYRVEDSVDWKVVDDVSNQTSCLAG 299
DB 241 VHVSRVGGLEDQLSVRVWSPPALKDFLQAKYQIRYRVEDSVDWKVVDDVSNQTSCLAG 300
QY 300 LKPGTVYFVQVRCNPFYGVSKKAGIWSGWSHPTAASPRSERPGPGGACPRGEPSS 359
DB 301 LKPGTVYFVQVRCNPFYGVSKKAGIWSGWSHPTAASPRSERPGPGGACPRGEPSS 360
QY 360 GVPRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP 419
DB 361 GVPRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGP 420
QY 420 AR 421
DB 421 AR 422
RESULT 8
AAG63545
ID AAG63545 standard; protein; 422 AA.
XX
XX AAG63545;
XX
XX 15-OCT-2001 (first entry)
XX
XX Amino acid sequence of a human CLF-1 protein.
XX
XX NNT-1; CLF-1; sCNTFalpha; nervous system; neuron; nervous system;
XX neuro muscular function; tumour; immune system; haematopoietic system;
XX reproductive system; liver; skeletal muscle; neurodegenerative disease;
XX amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;
XX muscular mass; paralysis; cancer; obesity; fertility; endometriosis;
XX blastocyst implantation; thrombosis; retinal disease;
XX retinal pigmentosis.

XX Homo sapiens.
 XX WO200155172-A2.
 XX 02-AUG-2001.
 XX 26-JAN-2001; 2001WO-FR000253.
 XX 27-JAN-2000; 2000FR-00001035.
 XX 12-OCT-2000; 2000FR-00013089.
 XX (FABR) FABRE MEDICAMENT SA PIERRE.
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
 XX WPI; 2001-488773/53.
 XX N-PSDB; AAH74486.
 XX A complex comprising a NNT-1 protein and a CLF-1 and/or scNTRalpha
 XX protein useful to treat neurodegenerative disease including Parkinson's
 XX and Huntington's, obesity and cancer.
 XX Claim 2; Page 63-64; 67pp; French.
 XX The present sequence represents a human CLF-1 protein. The specification
 XX describes a complex comprising a NNT-1 protein and a CLF-1 and/or
 XX scNTRalpha protein. The NNT-1/CLF-1 complex is used to modulate activity
 XX of the scNTRalpha/gpi30/LiFRbeta receptor complex, or to induce
 XX phosphorylation of the tyrosine of gpi30 and LiFRbeta, particularly where
 XX cells expressing the receptor complex are in the central or peripheral
 XX nervous system, in neurons implicated in neuro-muscular function or in
 XX skeletal muscle. The complex or antibodies are also used to decrease the
 XX survival, growth or proliferation of tumour cells or to facilitate the
 XX proliferation and/or inhibit differentiation of cells stocks. The complex
 XX is also used to modulate activity of the gpi30/LiFRbeta receptor or cells
 XX expressing that receptor, particularly those cells implicated in the
 XX immune, haematopoietic, nervous or reproductive system, the liver or
 XX skeletal muscle. Molecules of the invention may be used to prevent or
 XX treat neurodegenerative diseases including amyotrophic lateral sclerosis,
 XX Parkinson's and Huntington's disease, to repair or regenerate nervous or
 XX muscular tissue or to maintain muscular mass in paralysis patients. They
 XX may also be used to treat cancer, obesity and associated diseases, and to
 XX improve fertility, particularly to avoid endometriosis and/or assist
 XX blastocyst implantation, thrombosis, or retinal disease, particular
 XX retinal pigmentosis
 XX SQ Sequence 422 AA;
 Query Match 99.5%; Score 2279.5; DB 4; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3.9e-184;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 59
 DB 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 60
 QY 60 SVHGDDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
 DB 61 SVHGDDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 QY 120 GSILAGSCLYGLPPEKPNVISCWKNMKDLTCRWTPGAGHGETFLHTNYSKYKLRWYQ 179
 DB 121 GSILAGSCLYGLPPEKPNVISCWKNMKDLTCRWTPGAGHGETFLHTNYSKYKLRWYQ 180
 QY 180 DNTCEYHTVGHSHCHIPKDLALFTPYEIWVEATNRLSARSDDLTLDLVVTDDPPDD 239
 DB 181 DNTCEYHTVGHSHCHIPKDLALFTPYEIWVEATNRLSARSDDLTLDLVVTDDPPDD 240
 QY 240 VHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 299
 DB 241 VHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 300

QY 300 LKPGTVYFVQVRCNPFGIYGSKAGIWSHPTAASRPRSGPGGACERGGEPSS 359
 DB 301 LKPGTVYFVQVRCNPFGIYGSKAGIWSHPTAASRPRSGPGGACERGGEPSS 360
 QY 360 GPNRRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQDSEGLIPSGRRGTARGP 419
 DB 361 GPNRRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQDSEGLIPSGRRGTARGP 420
 QY 420 AR 421
 DB 421 AR 422
 RESULT 9
 ABUS5925
 ID ABUS5925 standard; protein; 422 AA.
 XX AC ABUS5925;
 XX 26-MAR-2003 (first entry)
 XX Human secreted/transmembrane protein PRO327.
 XX Human; PRO; secreted protein; transmembrane protein; anti-HIV;
 KW cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic;
 KW cardiatic; AIDS; acquired immunodeficiency syndrome; cancer;
 KW atherosclerosis; inflammatory disease; diabetic complication;
 KW cardiac injury; organ failure.
 XX Homo sapiens.
 OS US2002142959-A1.
 PN 03-OCT-2002.
 PD 31-AUG-2001; 2001US-00944654.
 PF 16-SEP-1998; 98WO-US019330.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-JUN-1999; 99WO-US012252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US00414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001US-00866028.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX WPI; 2003-174141/17.
 DR N-PSDB; ABX75462.
 XX New isolated PRO polypeptide and encoding nucleic acid, useful for the
 PT diagnosis and treatment of disorders associated with the PRO polypeptide,
 PT such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
 XX Claim 12; Fig 14; 178pp; English.
 XX The invention relates to an isolated PRO polypeptide (a secreted or
 CC transmembrane protein) comprising: (a) at least 80% sequence identity or

CC positives when compared to any of 15 sequences, fully defined in the
CC specification, lacking or with its associated signal peptide; or (b) at
CC least 80% sequence identity to a sequence encoded by the full-length
CC coding sequence of a DNA deposited in the American Type Culture
CC Collection (ATCC). Also included are: (1) an isolated nucleic acid
CC comprising: (a) at least 80% sequence identity to a nucleotide sequence
CC that encodes a PRO protein; (b) at least 80% sequence identity to a
CC nucleotide sequence or full-length coding sequence with any of 15 fully
CC defined sequences of 957-3441 base pairs, given in the specification; or
CC (c) at least 80% sequence identity to a full-length coding sequence of a
CC DNA deposited under ATCC Accession No. 209526, 209508, 209528,
CC 209530, 209523, 209492, 209532, 209531, 209529, 209527, 209570, 209618,
CC 209621 or 209619; (2) a vector comprising the nucleic acid; (3) a host
CC cell comprising the vector which, when cultured under conditions suitable
CC for expression of the PRO polypeptide, produces the PRO protein; (4) a
CC chimeric molecule comprising PRO fused to a heterologous amino acid
CC sequence; and (5) an anti-PRO antibody. The methods and compositions of
CC the present invention are useful for the diagnosis and treatment of
CC disorders associated with the PRO polypeptide, such as AIDS (acquired
CC immunodeficiency syndrome), cancer, atherosclerosis, inflammatory
CC disease, diabetic complications, cardiac injury and organ failure. The
CC antibodies can also be used in the different screening, therapeutic and
CC biological assays. The present sequence represents a PRO protein
XX
SQ Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSAGTAIVISPDPTLLIGSSLLATC 59
Db 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSAGTAIVISPDPTLLIGSSLLATC 60

QY 60 SVHGDDPPGATAGLYWTLNGRLPPPELSRVLANASTLALANLNGRSQNSLVCHARD 119
Db 61 SVHGDDPPGATAGLYWTLNGRLPPPELSRVLANASTLALANLNGRSQNSLVCHARD 120

QY 120 GSILAGSCLYVGLPPEKPNVISCWSKNMKDLTCRWTPGAGHETFLHTNYSKYKLRWYQ 179
Db 121 GSILAGSCLYVGLPPEKPNVISCWSKNMKDLTCRWTPGAGHETFLHTNYSKYKLRWYQ 180

QY 180 DNTCEYHTVGHSHCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVVTDDPPD 239
Db 181 DNTCEYHTVGHSHCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVVTDDPPD 240

QY 240 VHSVRYGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVSDSVDMKVVDVSNQTSCLAG 299
Db 241 VHSVRYGGLEDQLSVRWVSPPALKDFLQAKYQIRYRVSDSVDMKVVDVSNQTSCLAG 300

QY 300 LKPGTYVYFVQRCNPFYIGYKSKAGIWSWSHPTAATPRSERPGGGACPRGGEPS 359
Db 301 LKPGTYVYFVQRCNPFYIGYKSKAGIWSWSHPTAATPRSERPGGGACPRGGEPS 360

QY 360 GPVRELKQFLGWLKHAHCNSNLSFLYDQRAWMOKSHKTRNQDGIILPSGRGTARGP 419
Db 361 GPVRELKQFLGWLKHAHCNSNLSFLYDQRAWMOKSHKTRNQDGIILPSGRGTARGP 420

QY 420 AR 421
Db 421 AR 422

RESULT 10
ABU60235
ID ABU60235 standard; protein; 422 AA.
XX
AC ABU60235;
XX
DT 24-APR-2003 (first entry)
XX
DE Human PRO polypeptide #6.
XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer;
KW inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility;
KW birth defect; premature aging; diabetes; dog; cat; horse;
KW acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit;
KW industry; cytostatic; antiinflammatory; cardiant; antiinfectility;
KW anti-HIV; antiarteriosclerotic; antidiabetic.
XX
OS Homo sapiens.
XX
PN US2002132768-A1.
XX
PD 19-SEP-2002.
XX
PF 31-AUG-2001; 2001US-00945015.
XX
PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069702P.
PR 16-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-00216021.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 03-MAR-1999; 99US-00254311.
PR 22-JUN-1999; 99WO-US012252.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff B;
PI Gerritsen ME, Goddard A, Godowski FJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
DR WPI; 2003-174088/17.
DR N-PSDB; ABX89453.
XX
XX
PT New secreted and transmembrane polypeptides (e.g. PRO241, for use in
PT pharmaceuticals, diagnostics or bioreactors, particularly for detecting
PT or treating e.g. cancers, infertility or acquired immunodeficiency
PT syndrome in mammals.
XX
XX
XX Claim 1; Fig 14; 173pp; English.
XX
XX The invention relates to a human secreted and transmembrane polypeptide
XX (PRO) and the polynucleotide encoding it. The PRO polypeptide or
CC polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or

CC bioreactors. These are particularly useful for detecting or treating
CC cancers, inflammatory diseases, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, acquired immunodeficiency
CC syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs,
CC cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are
CC also useful in biotechnological and medical research and in various
CC industrial applications. Sequences ABU60230-ABU60245 represent human PRO
CC polypeptides of the invention
XX
SQ Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59
DB 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
QY 60 SVHGDPGATAGLYWTNLNRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
DB 61 SVHGDPGATAGLYWTNLNRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 179
DB 121 GSILAGSCLYVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 180
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVVTDDPPD 239
DB 181 DNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVVTDDPPD 240
QY 240 VHVSRVGGLEDQLSVRWVSPFALKDPLFQAKYQIRYRVEDSVDKVVDVDSNQTSCRLAG 299
DB 241 VHVSRVGGLEDQLSVRWVSPFALKDPLFQAKYQIRYRVEDSVDKVVDVDSNQTSCRLAG 300
QY 300 LKPGTVYFVQRCNPGIYVSKAGIWSWSHPTAASRPRPGGGACPRGGEPS 359
DB 301 LKPGTVYFVQRCNPGIYVSKAGIWSWSHPTAASRPRPGGGACPRGGEPS 360
QY 360 GPRRELKQFLGWLKHKYCSNLSFRLYDQWRAWQSHKTRNODGILPSSRRGTARGP 419
DB 361 GPRRELKQFLGWLKHKYCSNLSFRLYDQWRAWQSHKTRNODGILPSSRRGTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 11
ABG72776
XX ID ABG72776 standard; protein; 422 AA.
XX AC ABG72776;
XX DT 20-FEB-2003 (first entry)
XX DE Human cytokine receptor-like factor 1 (CLRF-1 or CLRF-1) protein.
XX KW Human; gene expression; bone formation; cartilage formation;
KW embryonic development; cytokine receptor-like factor 1; CLRF-1; CLRF-1;
KW mesenchymal cell differentiation; matrix metalloproteinase 23; MMP23;
KW bone development; antagonist; agonist; cadherin; CD68; cytokine;
KW diagnosis; osteodystrophy; osteohypertrophy; osteoblastoma;
KW osteopetrosis; osteogenesis imperfecta; osteoporosis; osteopenia;
KW osteoma; osteoblastoma; periodontal disease; hyperparathyroidism;
KW hypercalcaemia of malignancy; Paget's disease; osteolytic lesion;
KW bone metastasis; bone loss; immobilisation; sex hormone deficiency;
KW inflammatory disease; rheumatoid arthritis; osteoarthritis;
KW bone fracture.
XX OS Homo sapiens.
XX WO200285285-A2.
PN

XX PD 31-OCT-2002.
XX PF 18-APR-2002; 2002WO-US012149.
XX PR 18-APR-2001; 2001US-0284786P.
XX PA (AMHP) WYETH.
XX PI Clancy B, Pittman DM;
XX WPI: 2003-103384/09.
XX N-PSDB; ABX14013.
XX Determining the difference between levels of expression of a number of
XX genes, useful for diagnosing and treating disorders associated with bone
XX or cartilage formation or resorption such as osteoporosis and bone
XX fractures.
XX Disclosure; Page 192-193; 197pp; English.
XX The invention discloses a method for determining the difference between
XX the levels of expression of a number of, at least 500 genes, during bone
XX or cartilage formation. The method comprises determining levels of RNA
XX from the genes to obtain levels of expression and comparing these to a
XX set of reference levels for each of the genes. Bone formation is an
XX essential process in embryonic development and plays a critical role in
XX many diseases and conditions in humans. Two genes found to be regulated
XX during bone and cartilage formation are the cytokine receptor-like factor
XX 1 (CLRF-1 or CLRF-1), which is specifically regulated during mesenchymal
XX cell differentiation, and matrix metalloproteinase 23 (MMP23), which is
XX specifically regulated during bone development. Also disclosed is a
XX computer program for analysing levels of expression of a number of genes,
XX compositions comprising a number of antagonists or agonists of the genes
XX and methods for determining whether a subject has, or is likely to
XX develop, a disease related to bone or cartilage resorption or formation,
XX for determining the effectiveness of a treatment intended to stimulate
XX bone or cartilage formation or resorption, for identifying a compound for
XX treating, modulating or stimulating a disease related to bone or
XX cartilage formation possibly acting as a cadherin or CD68 agonist or a
XX cytokine antagonist. The methods and compositions are useful for
XX diagnosing and treating disorders associated with bone or cartilage
XX formation or resorption such as osteodystrophy, osteohypertrophy,
XX osteoblastoma, osteopetrosis, osteogenesis imperfecta, osteoporosis,
XX osteopenia, osteoma and osteoblastoma, periodontal disease,
XX hyperparathyroidism, hypercalcaemia of malignancy, Paget's disease,
XX osteolytic lesions produced by bone metastasis, bone loss due to
XX immobilisation or sex hormone deficiency, bone and cartilage loss caused
XX by an inflammatory disease, rheumatoid arthritis, osteoarthritis and bone
XX fractures. The sequence presented is the human CLF-1 protein
XX
SQ Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59
DB 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
QY 60 SVHGDPGATAGLYWTNLNRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
DB 61 SVHGDPGATAGLYWTNLNRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 179
DB 121 GSILAGSCLYVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQ 180
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVVTDDPPD 239
DB 181 DNTCEYHTVGPHSCHIPKDLALFTPEYIWEATNRLGARSDDLTLDLVVTDDPPD 240

QY 240 VHSVGVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVWVKVDDVSNQTSCLAG 299
DB 241 VHSVGVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVWVKVDDVSNQTSCLAG 300
QY 300 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASPRSRPGGACPRGGEPS 359
DB 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASPRSRPGGACPRGGEPS 360
QY 360 GPRRELKQFLGWLKKHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 419
DB 361 GPRRELKQFLGWLKKHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 420
QY 420 AR 421
DB 421 AR 422
RESULT 12
ABU64921
ID ABU64921 standard; protein; 422 AA.
XX AC ABU64921;
XX DT 15-MAY-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO327.
XX KW Human; PRO; secreted protein; transmembrane protein;
KW Cornelia de Lange syndrome; gene therapy; immune disorder;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
XX KW diabetic complication.
OS Homo sapiens.
XX PN US2002173463-A1.
XX PD 21-NOV-2002.
XX PF 31-AUG-2001; 2001US-00944944.
XX PR 03-DEC-1997; 97US-0067411P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 16-DEC-1997; 97US-0069694P.
PR 16-DEC-1997; 97US-0069696P.
PR 16-DEC-1997; 97US-0069702P.
PR 17-DEC-1997; 97US-0069870P.
PR 17-DEC-1997; 97US-0069873P.
PR 18-DEC-1997; 97US-0068017P.
PR 05-JAN-1998; 98US-0070440P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-FEB-1998; 98US-0075945P.
PR 16-SEP-1998; 98WO-US019330.
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 22-DEC-1998; 98US-0113296P.
PR 02-JUN-1999; 99WO-US012252.
PR 28-JUL-1999; 99US-0146222P.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.

PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX (GETH) GENENTECH INC.
XX PA Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
XX PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX WPI; 2003-311003/30.
DR N-PSDB; ABX96790.
XX New transmembrane polypeptides and polynucleotides useful for chromosome
PT identification, tissue typing, gene therapy, in chromosome and gene
PT mapping, or as molecular weight markers.
XX Claim 12; Fig 14; 172pp; English.
XX The invention relates to an isolated nucleic acid encoding a secreted/
CC transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and their encoding polynucleotides are disclosed. Also
CC included are a vector comprising the PRO nucleic acid, a host cell
CC comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
CC polypeptide, and recovering the PRO polypeptide from the cell culture, an
CC isolated polypeptide having at least 80% amino acid sequence identity to
CC the PRO polypeptides, a chimaeric molecule comprising PRO fused to a
CC heterologous amino acid sequence and an antibody which specifically binds
CC to PRO. The PRO nucleotide sequences are useful as hybridisation probes,
CC in chromosome and gene mapping, in generating sense and antisense RNA or
CC DNA, in generating transgenic or knock-out animals which can be used in
CC the development and screening of therapeutically useful reagents, and in
CC gene therapy. The polypeptides may be used as molecular weight markers
CC for protein electrophoresis purposes. The PRO polypeptides and nucleic
CC acids may also be used for chromosome identification, and tissue typing.
CC PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
CC syndrome. Other PRO proteins are variously implicated in immune
CC disorders, inflammatory disease, organ failure, atherosclerosis, cardiac
CC injury, infertility, birth defects, premature aging, cardiac injury,
CC AIDS, cancer and diabetic complications. The present sequence represents
CC a PRO protein
XX Sequence 422 AA;
SQ Query Match 99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAQARRPPPLLP-LLILCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 59
DB 1 MPAGRRGPAQAQARRPPPLLP-LLILCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
QY 60 SVHGDPPGATAGLYWTLNGRLPPELSRVLNASTLALANLNGSRQSGNVLVCHARD 119
DB 61 SVHGDPPGATAGLYWTLNGRLPPELSRVLNASTLALANLNGSRQSGNVLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHGTFLHTNYSLKYLWYQG 179
DB 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHGTFLHTNYSLKYLWYQG 180
QY 180 DNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLDLVVTTPPPD 239
DB 181 DNTCEYHTVGPHSCHIPKDLALFTPYEIWEATNRLGARSDDLTLDLVVTTPPPD 240
QY 240 VHSVGVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVWVKVDDVSNQTSCLAG 299
DB 241 VHSVGVGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVSDSVWVKVDDVSNQTSCLAG 300
QY 300 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASPRSRPGGACPRGGEPS 359
DB 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASPRSRPGGACPRGGEPS 360

QY 360 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGRTARGP 419
 Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGRTARGP 420
 QY 420 AR 421
 Db 421 AR 422

RESULT 13
 ABUS8355
 ID ABUS8355 standard; protein; 422 AA.
 XX
 AC ABUS8355;
 14-APR-2003 (first entry)
 XX
 DT Novel human secreted protein PRO327.
 DE
 XX
 KW Human; antiinflammatory; antiarteriosclerotic; cardiant; gynecological;
 KW anti-HIV; cytostatic; antidiabetic; BMP-agonist; gene-Therapy;
 KW cytokine-agonist; cytokine-antagonist; gene-Therapy;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defect; premature aging; AIDS; cancer;
 KW diabetic complication.
 XX
 OS Homo sapiens.
 XX
 XX
 PN US2002150976-A1.
 XX
 PD 17-OCT-2002.
 XX
 XX 30-AUG-2001; 2001US-00943851.
 XX
 PR 03-DEC-1997; 97US-0067411P.
 PR 11-DEC-1997; 97US-0069278P.
 PR 11-DEC-1997; 97US-0069334P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 16-DEC-1997; 97US-0069696P.
 PR 16-DEC-1997; 97US-0069702P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 17-DEC-1997; 97US-0069873P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 05-JAN-1998; 98US-0070440P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-00216021.
 PR 16-DEC-1998; 98US-0112850P.
 PR 22-DEC-1998; 98US-00218517.
 PR 22-DEC-1998; 98US-0113296P.
 PR 03-MAR-1999; 99US-00254311.
 PR 02-JUN-1999; 99WO-US012252.
 PR 28-JUL-1999; 99US-0146222P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001US-00866028.
 XX

PA (GETH) GENENTECH INC.
 XX Baker KP, Boetstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
 PI Hillan KJ, Kijavini LJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 DR WPI; 2003-198285/19.
 DR N-PSDB; ABX78444.
 XX
 XX New isolated PRO polypeptide and encoding nucleic acids, useful for the
 PT diagnosis and treatment of disorders such as inflammatory disease,
 PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
 PT complications.
 XX
 PS Claim 12; Fig 14; 171pp; English.
 XX
 CC The invention describes a novel isolated PRO polypeptide. The methods and
 CC compositions of the present invention are useful for the diagnosis and
 CC treatment of disorders such as inflammatory disease, organ failure,
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature
 CC aging, AIDS, cancer, diabetic complications and mutations in general.
 CC This is the amino acid sequence of a novel human secreted PRO protein
 XX
 XX Sequence 422 AA;
 SQ

Query Match 99.5%; Score 2279.5; DB 6; Length 422;
 Best Local Similarity 99.8%; Pred. No. 3.9e-184;
 Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLLP-LLLLCVLGAPRAGSAGTAIVISPODPTLLIGSSLLATC 59
 Db 1 MPAGRRGPAQAQARRPPPLLP-LLLLCVLGAPRAGSAGTAIVISPODPTLLIGSSLLATC 60
 QY 60 SVHGDPPGATAGLYWTLNGLRPPPELSRVLTALALANLNGSRQSDNVLVCHARD 119
 Db 61 SVHGDPPGATAGLYWTLNGLRPPPELSRVLTALALANLNGSRQSDNVLVCHARD 120
 QY 120 GSILAGSCLYVGLPPEKPVNISCKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQG 179
 Db 121 GSILAGSCLYVGLPPEKPVNISCKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQG 180
 QY 180 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWATNRLGARSADVLTLDILDVVTDDPPD 239
 Db 181 DNTCEYHTVGPHSCHIPKDLALFTPYEIVWATNRLGARSADVLTLDILDVVTDDPPD 240
 QY 240 VHSVGVGLEDQLSVRWVSPPALKDFLFOAKYQIYRVEDSVDMKVVDVSNQTSCLAG 299
 Db 241 VHSVGVGLEDQLSVRWVSPPALKDFLFOAKYQIYRVEDSVDMKVVDVSNQTSCLAG 300
 QY 300 LKPGTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASRPSRPPGGACBPRGGEPS 359
 Db 301 LKPGTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASRPSRPPGGACBPRGGEPS 360
 QY 360 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGRTARGP 419
 Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQDRGILPSGRGRTARGP 420
 QY 420 AR 421
 Db 421 AR 422

RESULT 14
 ABUS7241
 ID ABUS7241 standard; protein; 422 AA.
 XX
 AC ABUS7241;
 XX
 DT 04-APR-2003 (first entry)
 XX
 DE Human PRO327 protein.
 XX
 KW Human; antiinflammatory; antiarteriosclerotic; cardiant;

KW anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane;
 KW anti-inflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility;
 KW anti-infertility; cytostatic; antidiabetic; gene therapy; birth defect;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW premature aging; AIDS; cancer; diabetic complication.

XX Homo sapiens.

XX US2002142958-A1.

XX 03-OCT-2002.

XX 30-AUG-2001; 2001US-00943762.

XX 16-SEP-1998; 98WO-US019330.

XX 01-DEC-1998; 98WO-US025108.

XX 22-JUN-1999; 99WO-US012252.

XX 15-SEP-1999; 99WO-US021090.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 16-DEC-1999; 99WO-US030095.

XX 11-FEB-2000; 2000WO-US003565.

XX 22-FEB-2000; 2000WO-US004414.

XX 02-MAR-2000; 2000WO-US005841.

XX 30-MAR-2000; 2000WO-US006439.

XX 22-MAY-2000; 2000WO-US014042.

XX 28-JUL-2000; 2000WO-US020710.

XX 01-DEC-2000; 2000WO-US032678.

XX 28-FEB-2001; 2001WO-US006520.

XX 25-MAY-2001; 2001US-00866028.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;

XX Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;

XX Hillan KJ, Kljavin LJ, Napier MA, Roy MA, Tumas D, Wood WI;

XX N-PSDB; ABX77077.

XX WPI; 2003-174140/17.

XX N-PSDB; ABX77077.

XX New secreted and transmembrane nucleic acids and polypeptides, designated

XX as PRO, useful for treating inflammation, organ failure, atherosclerosis,

XX cardiac injury, infertility, birth defects, premature aging, AIDS, or

XX cancer.

XX Claim 1; Fig 14; 173pp; English.

XX This invention relates to a nucleotide sequence encoding an isolated

XX secreted and/or transmembrane protein. The nucleotide sequences of the

XX invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti

XX -infertility, anti-HIV, cytostatic and antidiabetic activities and may be

XX used in gene therapy. The nucleic acids and polypeptides are useful for

XX treating inflammatory diseases, organ failure, atherosclerosis, cardiac

XX injury, infertility, birth defects, premature aging, AIDS, cancer, or

XX diabetic complications. The nucleic acids are useful as hybridisation

XX probes, in chromosome and gene mapping, and in generating antisense RNA

XX or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,

XX biosensors or bioreactors. Both are useful in tissue typing. The present

XX sequence represents a protein encoded by the nucleic acids of the

XX invention

XX

SQ Sequence 422 AA;

Query Match 99.5%; Score 2279.5; DB 6; Length 422;

Best Local Similarity 99.8%; Pred. No. 3.9e-184;

Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 MPAGRGRPAQAARRPPPLP-ILLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59

1 MPAGRGRPAQAARRPPPLP-ILLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60

60 SVHGDPPGATAGLYWTNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 119

Db 61 SVHGDPPGATAGLYWTNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 120
 QY 120 GSILAGSCLYVGLPPEKPNVSCSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYQ 179
 Db 121 GSILAGSCLYVGLPPEKPNVSCSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYQ 180
 QY 180 DNTCEEYHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDLVVTDDPPD 239
 Db 181 DNTCEEYHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDLVVTDDPPD 240
 QY 240 VHSVSVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 299
 Db 241 VHSVSVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 300
 QY 300 LKPGTVYFVQVRCNPFYIGSKKAGIWEWSHPTAASPRSRPFGGGACPRGGEPS 359
 Db 301 LKPGTVYFVQVRCNPFYIGSKKAGIWEWSHPTAASPRSRPFGGGACPRGGEPS 360
 QY 360 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPSGRGTARGP 419
 Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPSGRGTARGP 420
 QY 420 AR 421
 Db 421 AR 422
 RESULT 15
 ABUS6306
 ID ABUS6306 standard; protein; 422 AA.
 XX AC ABUS6306;
 XX DT 31-MAR-2003 (first entry)
 XX DE Human secreted/transmembrane protein, PRO327.
 XX KW Human; PRO; antiinflammatory; antiarteriosclerotic; cardiant;
 KW gynecological; anti-HIV; cytostatic; antidiabetic; inflammatory disease;
 KW organ failure; atherosclerosis; cardiac injury; infertility;
 KW birth defect; premature aging; AIDS; acquired immunodeficiency syndrome;
 KW cancer; diabetic complication.
 XX OS Homo sapiens.
 XX PN US2002132981-A1.
 XX PD 19-SEP-2002.
 XX PF 30-AUG-2001; 2001US-00944396.
 XX PR 03-DEC-1997; 97US-0067411P.
 PR 11-DEC-1997; 97US-0069278P.
 PR 11-DEC-1997; 97US-0069334P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 16-DEC-1997; 97US-0069696P.
 PR 16-DEC-1997; 97US-0069702P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 17-DEC-1997; 97US-0069873P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 05-JAN-1998; 98US-0070408P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 16-SEP-1998; 98WO-US019330.
 PR 01-DEC-1998; 98WO-US025108.
 PR 16-DEC-1998; 98US-0112850P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 28-JUL-1999; 99US-0146222P.

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PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 25-MAY-2001; 2001US-00866028.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
PI Hillian KJ, Kijavini IJ, Napier MA, Roy MA, Tumas D, Wood WI;
XX
XX WPI; 2003-147446/14.
XX N-PSDB; ABX75909.
XX
XX New isolated PRO polypeptide and encoding nucleic acids, useful for the
PT diagnosis and treatment of disorders such as inflammatory disease,
PT atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
PT complications.
XX
XX Claim 12; Fig 14; 17lpp; English.
XX
XX The invention relates to an isolated PRO polypeptide having at least 80%
CC amino acid sequence identity to and scoring at least 80% positives when
CC compared to any of 15 fully defined sequences of 235-954 amino acids,
CC given in the specification. Also included are: (1) an isolated PRO
CC nucleic acid having at least 80% nucleic acid sequence identity to a
CC nucleotide sequence that encodes PRO or its extracellular domain, and
CC comprising any of 15 fully defined nucleotide sequences of 957-3441 bp,
CC given in the specification and deposited under ATCC accession number
CC 209526, 209508, 209528, 209530, 209523, 209492, 209532, 209531,
CC 209529, 209527, 209570, 209618, 209621 and 209619; (2) a vector
CC comprising the PRO nucleic acid; (3) a host cell comprising the vector;
CC (4) producing PRO polypeptides, comprising culturing the cell for
CC expression of the PRO polypeptide and recovering the PRO polypeptide from
CC the cell culture; (5) a chimaeric molecule comprising PRO fused to a
CC heterologous amino acid sequence; and (6) an anti-PRP antibody. The
CC methods and compositions are useful for the diagnosis and treatment of
CC disorders such as inflammatory disease, organ failure, atherosclerosis,
CC cardiac injury, infertility, birth defects, premature aging, AIDS
CC (acquired immunodeficiency syndrome), cancer, diabetic complications and
CC mutations in general. The present sequence is a PRO polypeptide
XX
XX Sequence 422 AA;
```

```
Query Match          99.5%; Score 2279.5; DB 6; Length 422;
Best Local Similarity 99.8%; Pred. No. 3.9e-184;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGFAAQAARPPPLP-LLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 59
DB 1 MPAGRRGFAAQAARPPPLP-LLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 60
QY 60 SVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRSGDNLVCHARD 119
DB 61 SVHGDPGATAGLWTLNGRLPPELSRVLNASTLALANLNGSRSGDNLVCHARD 120
QY 120 GSILAGSCLYVGLPEKPNVSCSKNMKDLTCRWTPGAGHGETFLHTNYSKYLKRWYQ 179
DB 121 GSILAGSCLYVGLPEKPNVSCSKNMKDLTCRWTPGAGHGETFLHTNYSKYLKRWYQ 180
QY 180 DNTCEYHTVGHSCHPKDLALFTPYEHWIWEATNRLGARSDDLTLIDVWTTDPPPD 239
DB 181 DNTCEYHTVGHSCHPKDLALFTPYEHWIWEATNRLGARSDDLTLIDVWTTDPPPD 240
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Search completed: April 11, 2006, 02:09:57
Job time : 116.031 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 02:10:19 ; Search time 21.0667 Seconds
(without alignments)
1922.808 Million cell updates/sec

Title: US-09-037-657-44
Perfect score: 2290
Sequence: 1 MPAGRRGPAQASARPPPLL.....NODEILPSGRRGTARGPAR 421

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	332	14.5	288	B59405	prolactin receptor
2	332	14.5	376	A59405	prolactin receptor
3	332	14.5	622	A40144	prolactin receptor
4	323	14.1	918	A36337	membrane glycoprot
5	317.5	13.9	917	I49699	glycoprotein 130 -
6	316	13.8	830	I50455	prolactin receptor
7	314.5	13.7	918	A44257	interleukin-6 sign
8	313	13.7	310	A29884	prolactin receptor
9	313	13.7	412	A41070	prolactin receptor
10	313	13.7	610	A34631	prolactin receptor
11	313	13.7	610	A36116	prolactin receptor
12	309.5	13.5	292	I77524	prolactin receptor
13	309.5	13.5	303	I77524	prolactin receptor
14	309.5	13.5	608	I53269	prolactin receptor
15	308	13.4	831	QJ1655	prolactin receptor
16	306.5	13.4	581	I45971	prolactin receptor
17	300.5	13.1	616	A30304	prolactin receptor
18	263.5	11.5	630	I51086	prolactin receptor
19	255.5	11.2	837	A34898	granulocyte colony
20	249	10.9	372	I58141	ciliary neurotroph
21	242.5	10.6	771	B38252	granulocyte colony
22	242.5	10.6	783	JH0329	granulocyte colony
23	242.5	10.6	863	C38252	granulocyte colony
24	236	10.3	372	UHHUCN	ciliary neurotroph
25	211.5	9.2	362	S60614	growth promoting a
26	211.5	9.2	422	I37891	interleukin-11 rec
27	208.5	9.1	432	I48343	interleukin-11 rec
28	201	8.8	468	A41242	interleukin-6 rece
29	200	8.7	1097	S17308	leukemia inhibitor

30	199.5	8.7	460	2	JL0145	interleukin-6 rece
31	199	8.7	156	2	A32868	prolactin receptor
32	194.5	8.5	805	2	S68441	leptin receptor, s
33	194.5	8.5	892	2	S68439	leptin receptor, s
34	194.5	8.5	894	2	S68437	leptin receptor, s
35	194.5	8.5	900	2	S68440	leptin receptor, s
36	194.5	8.5	1162	2	S68438	leptin receptor, s
37	194	8.5	625	2	S35317	hematopoietic grow
38	191.5	8.4	440	2	JL0144	interleukin-6 rece
39	191	8.3	150	2	B34631	lactogen receptor
40	190.5	8.3	1162	2	PC4184	leptin receptor, O
41	190	8.3	626	2	S37622	proto-oncogene - m
42	187	8.2	1092	2	JM0312	differentiation-ac
43	186.5	8.1	579	2	B45266	MPL-K protein prec
44	186.5	8.1	635	2	A45266	MPL-P protein prec
45	184	8.0	895	2	S74225	leptin receptor, i

ALIGNMENTS

RESULT 1
B59405
prolactin receptor short form Sib precursor, breast cancer cells T-47D - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: B59405; B49400
R:Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A:Title: Isolation and characterization of two novel forms of the human prolactin recep
A:Reference number: A59405; MUID:21538812; PMID:11518703
A:Accession: B59405
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <HU>
A:Cross-references: UNIPROT:Q96P36; UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1
R:Hu, Z.Z.
Submitted to GenBank, December, 1999
A:Reference number: A49400
A:Accession: B49400
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <HU2>
A:Cross-references: UNIPARC:UPI000006CDDA; GB:AF214012; PIDN:AF214012.1
C:Comment: This is one of the short forms (Sia and Sib) of the human prolactin receptor ,
ta-casain gene promoter activation, with Sib more effective than Sia. However, their li
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-288/Product: prolactin receptor, short form Sib #status predicted <MAY>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 14.5%; Score 332; DB 2; Length 288;
Best Local Similarity 37.1%; Pred No. 1.7e-18;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 122 ILAGSCLYVG-LPPKPVNISCSNMKDLTCRWTFGAHGETFLHTNYSLKYLRYGQD 180
Db 15 LFLNLTCLLNGQLPPCKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTVHREGETLM 72
QY 181 NTCSEYHTVGHSCSHIPKD-LALFPTYEIWVEATWRLGSARSDVLTLDLDVVTDPDPD 239
Db 73 HECPDYITGGPNSCHFGKYTSMWRTYIMMVNATNMGSSPSDELYVDVYTVYVQDPPLPLE 132
QY 240 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVSDVSVMKVVDDVSNQTS 294
Db 133 LAV-EVKQPEDRKPYLWIKWSPTLIDLKTGHTFTLLYELRLKPEKAAWE-IHFAGQQTE 190
QY 295 CRLAGLKPGTVYFVQVRNCPFGIYGSKKAGIWSNSHPTAASTP 338


```
Db 91 FTDIASLNTQLTCNLTITLQGLBQNVYGITIISGLPEKPKNLSCIVNEGKXRCEDGGR 150
Qy 159 HGETFLHTNYSKYLKRWYQDNTCEVEYHTVGPSPHSCHIPKDLALFTPYEIVWEATNRLGS 218
Db 151 --ETHLETNFTLKSEWATHKPADCKAKRT--PTSCVTVDYSIVYFVNIWVWEAENALGK 206
Qy 219 ARSDVLTLDILDVVTTPDPDVHVSXVGLGDLQSVRVVSPALPKDFLFOAKYQIRYRVE 278
Db 207 VTSDDHINFDPVYKVPNPPHNLVINSEBLSLTKLTWN-PSIKSVII-LKYNIQYRTK 264
Qy 279 DSDVKKV---DDVSNQTSCLAGKPGYVYFVQVRCNPPFGIYGSKAGIWSHSPHAA 335
Db 265 DASTWSQIPPEPTASTRSFTVDLKPFTFYFRIRC-----MKEDGKGYSWDSERASG 319
Qy 336 STPRSERP 343
Db 320 IT-YEDRP 326

RESULT 5
I49699
Glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I49699; I48370
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:192291532; PMID:1602143
A:Accession: I49699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: UNIPROT:Q00560; UNIPARC:UPI000002845A; GB:M83336; NID:G193591; PIDN:
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RE2>
A:Cross-references: UNIPARC:UPI000002845A; EMBL:X62646; NID:G840816; PIDN:CAA44515.1; PI
C:Genetics:
A:Gene: gp130
C:Keywords: Glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 13.9%; Score 317.5; DB 2; Length 917;
Best Local Similarity 29.6%; Pred. No. 9.7e-17;
Matches 92; Conservative 50; Mismatches 146; Indels 23; Gaps 10;

Qy 42 ISPDQPTLLIGSSLLATCSVHG---DPPGATAEGLYWTNLGRRLPPELSRVLNASTLALA 98
Db 31 IYPEFPVQVQSGNFTACIVLKEACLOHYVYNASIVWKTNHAAPREQVTVNRTTSVT 90
Qy 99 LANLNGSRQRSGDNLVCHARDGSLIAGSLCYVGLPPEKPVNISCSWKMDLTCTRWTPCA 158
Db 91 FTDVVLPSVQLTCSNLLSFQGIQEQNVGVVTMLGFFPDKPTNLTCIVNEGKMLCQWDGPR 150
Qy 159 HGETFLHTNYSKYLKRWYQD-NTCEEYHTVGPSPHSCHIPKDLALFTPYEIVWEATNRLG 217
Db 151 --ETYLETNTYTLKSE--WATEKFPQCQSKHGT---SCWVSVMPTTYVNIWVWEAENALG 203
Qy 218 SARSDVLTLDILDVVTTPDPDVHVSXVGLGDLQSVRVVSPALPKDFLFOAKYQIRYRV 277
Db 204 KYSSSEINFDPVKDKPTFPYVNLVSNSELSLKLISWSSGL--GGLLDKSLDIQVRT 261
Qy 278 EDSVDWKV---DDVSNQTSCLAGKPGYVYFVQVRCNPPFGIYGSKAGIWSHSPHTA 334
Db 262 KDASTWIQVPLEDTWSPRTSFTVDLKPFTFYFRIR----SIKSGK-GYWSDSERAS 316
Qy 335 AST--PRSERP 343
Db 317 GTTYEDRPSPR 327
```

```
RESULT 6
I50455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267; PMID:7516866
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHS>
A:Cross-references: UNIPROT:Q90374; UNIPARC:UPI0000132233; EMBL:U07694; NID:G466381; PI
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 13.8%; Score 316; DB 2; Length 830;
Best Local Similarity 36.6%; Pred. No. 1.1e-16;
Matches 75; Conservative 30; Mismatches 82; Indels 18; Gaps 8;

Qy 133 PPEKPVNISCSWKMDLTCTRWTPGAHGETFLH-TNYSLKYLKRWYQDNTCEEYHTVGP 191
Db 231 PPEKPTIIKCRSPEKETFTCWKPGSDG--HPTNVTLLYSKEGEERYVECPDYKTAGP 287
Qy 192 HSCHI-PKDLALFTPYEIVWEATNLSGARSVDLTLDILDVVTTPDPDV--HVSXVGL 248
Db 288 NSCYFDKXHTSPWTIYNTVTKATNIGSNVDPLVDTYIVQTPPVNVTLELKKTVNR 347
Qy 249 EDQLSVRVVSPALKDF---LFQAKYQIRYRVSDVDWKVVDVSNQTSCLAGLKPQTV 305
Db 348 KPYLVLTW-SPPLADVRSGLTLDLYELRLKEPEAEWETI-FVQQTHYKMFSLNPGKK 405
Qy 306 YFVQVRCNPPFGIYGSKAGIWSWS 330
Db 406 YIVQIHCKP-----DHHGWSWSWS 424

RESULT 7
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.B.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducin
A:Reference number: A44257; MUID:93052397; PMID:1427893
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Cross-references: UNIPROT:P40190; UNIPARC:UPI000012D4D8
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 314.5; DB 2; Length 918;
Best Local Similarity 29.7%; Pred. No. 1.7e-16;
Matches 93; Conservative 51; Mismatches 140; Indels 29; Gaps 11;

Qy 42 ISPDQPTLLIGSSLLATC-----SVHGDPPGATAEGLYWTNLGRRLPPELSRVLNAST 94
Db 31 IYPEFPVQVQSGNFTATCVLKEKCLQVY---SVNATYVWKTNHAAPREQVTVNRTA 86
Qy 95 LALALANLNGSRQRSGDNLVCHARDGSLIAGSLCYVGLPPEKPVNISCSWKMDLTCTRW 154
Db 87 SSVTFTDVVFQNVQVQITCNILSFQGIQEQNVYGITILSGYPPDIPITNLSCIVNEGKMLCQL 146
Qy 155 TPGAHGETFLHTNYSKYLKRWYQD-NTCEEYHTVGPSPHSCHIPKDLALFTPYEIVWEAT 213
```

Db 147 DGR--EYLENYILKSE--WATEKFPDCRTH--GTSSCMGYTPYFVNIEVVAE 200
QY 214 NRGARSVDLFDILDVTTDPPDPVHVSRYGGLDQLSVRWSPALKDPLFOAKYOI 273
Db 201 NALGNVSSPINFDPVKPSPPHNLSVTNSEELSSILKLAWNSGL--DSILRLKSDI 258
QY 274 RYRVSDVDKVV---DDVSNOTSRLAGLKPGTYVFQVRCNPGIYGSKKAGIWSWS 330
Db 259 QYRTKDASTWIQVPLEDTVSPRTSFTVQDLKPFTEYVFRIR----SIXENGK-GYKWSOWS 313
QY 331 HPTAASTPRSERP 343
Db 314 E-EASGTYYEDRP 325
RESULT 8
A29884
prolactin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: A29884
R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ederly, M.; Shiota, M.; Banville
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A:Reference number: A29884; MUID:88165059; PMID:2832068
A:Accession: A29884
A:Molecule type: mRNA
A:Residues: 1-310 <BOU>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19A; GB:M19304; NID:g206364; PIDN:
C:Keywords: transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-310/Product: prolactin receptor #status predicted <MAT>
F:31-216/Domain: cytokine receptor homology <CRS>
Query Match 13.7%; Score 313; DB 2; Length 310;
Best Local Similarity 35.0%; Pred. No. 5.7e-17;
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;
QY 121 SILAGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSLKYLKWYGOD 180
Db 15 SLKKGQS-----PPGKPEIHKCRSPDKETFTCWNPPTDGG--LPNYSLSYSKE--GEK 65
QY 181 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTDLIDVTTDPP 237
Db 66 TTVECPDYKTSGPSNCFKQVTSIWKIYIITVNATNQMGSSSDPLYVDVTYIIVEPEPP 125
QY 238 PDVHVSRYGGLDQLSVRWV--SPALKDF---LFQAKYQIYRVVEDSDVKVDDVSNQ 292
Db 126 RNLTLL-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPEAEWE--IHFTGHQ 183
QY 293 TSCRLAGLKPGTYVFQVRCNPGIYGSKKAGIWSWSHPTAASP 338
Db 184 TQKVFDPGLPGQKYLVTQCKP-----DHGYNSRWSQESSVEMP 222
RESULT 9
A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41070; I55417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolact
A:Reference number: A41070; MUID:92041834; PMID:1718958
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI000002B19B; GB:M74152; NID:g206389; PIDN:
R'O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor

A:Reference number: I55417; MUID:95014432; PMID:7929319
A:Accession: I55417
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: UNIPARC:UPI000002B19B; EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PI
A:Experimental source: Nb2-11C cell line
C:Keywords: transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>
Query Match 13.7%; Score 313; DB 2; Length 412;
Best Local Similarity 35.0%; Pred. No. 8.1e-17;
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;
QY 121 SILAGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSLKYLKWYGOD 180
Db 15 SLKKGQS-----PPGKPEIHKCRSPDKETFTCWNPPTDGG--LPNYSLSYSKE--GEK 65
QY 181 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTDLIDVTTDPP 237
Db 66 TTVECPDYKTSGPSNCFKQVTSIWKIYIITVNATNQMGSSSDPLYVDVTYIIVEPEPP 125
QY 238 PDVHVSRYGGLDQLSVRWV--SPALKDF---LFQAKYQIYRVVEDSDVKVDDVSNQ 292
Db 126 RNLTLL-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPEAEWE--IHFTGHQ 183
QY 293 TSCRLAGLKPGTYVFQVRCNPGIYGSKKAGIWSWSHPTAASP 338
Db 184 TQKVFDPGLPGQKYLVTQCKP-----DHGYNSRWSQESSVEMP 222
RESULT 10
A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C:Accession: A34631
R:Zhang, R.; Buczek, B.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A:Reference number: A34631; MUID:90241201; PMID:2159291
A:Accession: A34631
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <ZHA>
A:Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170B1; GB:M34083; NID:g205122; PIDN
A>Note: the authors translated the codon GAG for residue 533 as Gly
F:31-216/Domain: cytokine receptor homology <CRS>
Query Match 13.7%; Score 313; DB 2; Length 610;
Best Local Similarity 35.0%; Pred. No. 1.3e-16;
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;
QY 121 SILAGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSLKYLKWYGOD 180
Db 15 SLKKGQS-----PPGKPEIHKCRSPDKETFTCWNPPTDGG--LPNYSLSYSKE--GEK 65
QY 181 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTDLIDVTTDPP 237
Db 66 TTVECPDYKTSGPSNCFKQVTSIWKIYIITVNATNQMGSSSDPLYVDVTYIIVEPEPP 125
QY 238 PDVHVSRYGGLDQLSVRWV--SPALKDF---LFQAKYQIYRVVEDSDVKVDDVSNQ 292
Db 126 RNLTLL-EVKQLDKKTYLWVKWSPPTITDVKTGWFTMEYIIRLKPEAEWE--IHFTGHQ 183
QY 293 TSCRLAGLKPGTYVFQVRCNPGIYGSKKAGIWSWSHPTAASP 338
Db 184 TQKVFDPGLPGQKYLVTQCKP-----DHGYNSRWSQESSVEMP 222
RESULT 11
A36116
prolactin receptor 2 precursor - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36116
R;Shioto, M.; Banville, D.; Ali, S.; Jolicœur, C.; Boutin, J.M.; Edery, M.; Djiane, J.
Mol. Endocrinol. 4, 1136-1143, 1990
A;Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A;Reference number: A36116; MUID:91155946; PMID:2293022
A;Accession: A36116
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-610 <SHI>
A;Cross-references: UNIPROT:P05710; UNIPARC:UPI0000170ADB; GB:M57668; NID:g206366; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.7%; Score 313; DB 2; Length 610;
Best Local Similarity 35.0%; Pred. No. 1.3e-16;
Matches 79; Conservative 36; Mismatches 85; Indels 26; Gaps 10;

QY 121 SLLAGSLVGLPPEKPVNISCSKMKDLTCWTPGAHGETFLHTNYSKYKLRWYQGD 180
DB 15 SLLKGS-----PPGKPEIHKCRSPDKETTCWNNFGTDG--LPTNYSLTYSKE--GSK 65

QY 181 NT--CEYHTVGPCHPKD-LALPTPEIWEATNRLGARSVDLTLDLDVTTDPP 237
DB 66 TTYECPDYKTSNPSCFPSKQYTSIWKIYIITVATNMGSSSDPLYVDVTIPEPP 125

QY 238 PDVHVSRLGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDVDKVVDDVSNQ 292
DB 126 RNLT-L-EVKQLDKKTYLWVKSPPITDVKTGFTWEYIRLKPAAEWE-IHFTGHQ 183

QY 293 TSCRLAGLPGTYVFOVRCNPGIYGSKAGIWSWSHPTAASP 338
DB 184 TQFKVFDLYPGQKYLVTQCKP-----DHGYWSRSQESSVEMP 222

RESULT 12
I77525
prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I77525
R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the prolactin receptor in mouse liver.
A;Reference number: I57699; MUID:89261824; PMID:2725531
A;Accession: I77525
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-292 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B198; GB:M22959; NID:g200481; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 309.5; DB 2; Length 292;
Best Local Similarity 31.4%; Pred. No. 9.9e-17;
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 86 LSRVLNASTLALANLNGSRQSGDNLVCHARDGSILAGSLYVGLPPEKPVNISCSWK 145
DB 1 MSSALAYMLLVLSISLNGQS-----PPGKPEIHKCRSP 34

QY 146 NMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNT--CEYHTVGPCHPKD-LAL 202
DB 35 DKETFTCMWNPSSDGG--LPTNYSLTYSKE--GKNTYECPDYKTSNPSCFPSKQYTSI 90

QY 203 FFPYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSRLGLEDQLSVRWVS--PP 260
DB 91 WKIYIITVATNMGSSSDPLYVDVTIPEPPRNLT-L-EVKQLDKKTYLWVKWLP 149

RESULT 13
I77524
prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I77524
R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the prolactin receptor in mouse liver.
A;Reference number: I57699; MUID:89261824; PMID:2725531
A;Accession: I77524
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-303 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI000002B197; GB:M22958; NID:g200479; PIDN:
F;31-216/Domain: cytokine receptor homology <CRS>

Query Match 13.5%; Score 309.5; DB 2; Length 303;
Best Local Similarity 31.4%; Pred. No. 1e-16;
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 86 LSRVLNASTLALANLNGSRQSGDNLVCHARDGSILAGSLYVGLPPEKPVNISCSWK 145
DB 1 MSSALAYMLLVLSISLNGQS-----PPGKPEIHKCRSP 34

QY 146 NMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNT--CEYHTVGPCHPKD-LAL 202
DB 35 DKETFTCMWNPSSDGG--LPTNYSLTYSKE--GKNTYECPDYKTSNPSCFPSKQYTSI 90

QY 203 FFPYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSRLGLEDQLSVRWVS--PP 260
DB 91 WKIYIITVATNMGSSSDPLYVDVTIPEPPRNLT-L-EVKQLDKKTYLWVKWLP 149

RESULT 14
I53269
prolactin receptor, long form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I53269; JT0671; S34356
R;Clarke, D.B.; Linzer, D.I.H.
Endocrinology 133, 224-232, 1993
A;Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
A;Reference number: I53269; MUID:93307149; PMID:8319571
A;Accession: I53269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-608 <RES>
A;Cross-references: UNIPROT:Q08501; UNIPARC:UPI0000020E90; GB:L14811; NID:g293769; PIDN:
R;Moore, R.C.; Oka, T.
Gene 134, 263-265, 1993
A;Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
A;Reference number: JT0671; MUID:94085788; PMID:8262385
A;Accession: JT0671
A;Molecule type: mRNA
A;Residues: 1-608 <MOO>
A;Cross-references: UNIPARC:UPI0000020E90; GB:L13593; NID:g347398; PIDN:AAC37641.1; PID
R;Edery, M.; Peret, A.; Nandi, S.; Kelly, P.A.
submitted to the EMBL Data Library, June 1993
A;Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
A;Reference number: S34356

A:Accession: S34356
A:Molecule type: mRNA
A:Residues: 1-557, 'F', 559-608 <EDE>
A:Cross-references: UNIPARC:UPI0000163B24; EMBL:X73372; NID:G312696; PIDN:CAAS1789.1; PI
C:Comment: Prolactin receptor have long form and short form which are resulted from alte
C:Comment: This long form receptor is capable of transducing a signal to milk protein ge
C:Keywords: receptor; transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>
F:230-253/Domain: transmembrane #status predicted <TMM>

Query Match 13.5%; Score 309.5; DB 2; Length 608;
Best Local Similarity 31.4%; Pred. No. 2.5e-16;
Matches 82; Conservative 38; Mismatches 94; Indels 47; Gaps 10;

QY 86 LSRVLNASTLALANLNGSRQRSGDNLVCHARDGSLAGSLYGLPEKPVNISCWSK 145
Db 1 MSSALAYMLLVLSILNQS-----PPKPEIHKCRSP 34

QY 146 NMKDLTCRWTPGAHGETFLHTNYSKYKLRTYQDNT--CEYHTVGHPSCHIPKD-LAL 202
Db 35 DKETETCWNPGSDG--LPTNYSLTYSKE--GEKNTECPDYKTSGPNSCFFSKYQYTSI 90

QY 203 FTFYEIWEATNRLGARSVDLTLDLDVVTTPDPDVHVSVRVGGLEDOLSVRWVS--PP 260
Db 91 WKYIITVNATNEMSGSTSDPLYVDVTVYVEPEPPRNLT-L-EVKQLKDKKTYLWKNLPP 149

QY 261 ALKDF---LFQAKYQIRYRVESVDWKVDDVSNQTSCLAGLKEGTTFYFVQVRCNPFGI 317
Db 150 TITDVKTGWFTMEYELRLKSEADEWE-IHFTGHQTQFKVFDLYPGQKYLVTQCKP--- 205

QY 318 YGSKKAGIWSWESHPTAAATP 338
Db 206 ----DHGYWSRMGQEKSIPI 222

RESULT 15
JQ1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A:Reference number: JQ1655; MUID:93075121; PMID:1445292
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: UNIPROT:Q04594; UNIPARC:UPI0000132232; DDBJ:D13154; NID:G222848; PII
A:Experimental source: kidney
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TMM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (coval
Query Match 13.4%; Score 308; DB 2; Length 831;
Best Local Similarity 34.6%; Pred. No. 4.7e-16;
Matches 75; Conservative 28; Mismatches 96; Indels 18; Gaps 8;

QY 133 PPEKPVNISCSNMKDLTCRWTPGAHGETFLH-TNYSKYKLRTYQDNTCEYHTVGP 191
Db 230 PPEKPTIHKCRSEKETFTCWKPGLDG--HPTNVTLLYSKEGEEQVVECPDYRTAGP 286

QY 192 HSCHI-PKDLALFTPEYIWEATNRLGARSVDLTLDLDVVTTPDPDV--HVSVRVGG 248
Db 287 NSCYFDKKHTSFWTYITNITRATNEMSGNSDPHYVDVTVYIVQDPFPVNTLELKKPINR 346

QY 249 EDOLSVRWVSPPAKQDF--LFQAKYQIRYRVESVDWKVDDVSNQTSCLAGLKEGTV 305
Db 347 KPYLVLTW-SPPPLADVRSGWLTLEELRLKPEGEWEYI-FVGQOTQYKMFSLNPGKK 404

QY 306 YFVQVRCNPFGLYSGKKAGIWSWESHPTAAATPRSER 342
Db 405 YIIQIHCKP-----DHHGWSWSSSENYIQIPNDFR 435

Search completed: April 11, 2006, 02:17:27
Job time : 22.0667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:04:23 ; Search time 125.397 Seconds
(without alignments)
2368.694 Million cells updates/sec

Title: US-09-037-657-44
Perfect score: 2290
Sequence: 1 MPAGRRGPAQAQARRPPPLL.....NQDEGILSGRRGTARGPAR 421

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_treml.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2279.5	99.5	422	1 CRLF1_HUMAN	Q75462 homo sapien
2	2178	95.1	425	1 CRLF1_MOUSE	Q9jms8 mus musculus
3	1418.5	61.9	389	2 Q6DG28_BRARE	Q6dg28 brachydanio
4	1384.5	60.5	394	2 Q6UAQ5_TETNG	Q6uaq5 tetraodon n
5	994	43.4	437	2 Q4RMP5_TETNG	Q4rmp5 tetraodon n
6	466.5	20.4	207	2 Q4TCM7_TETNG	Q4tcm7 tetraodon n
7	406	17.7	151	2 Q4RDR1_TETNG	Q4rdr1 tetraodon n
8	380	16.6	199	2 Q4RDQ9_TETNG	Q4rdq9 tetraodon n
9	365.5	16.0	918	2 Q9W6U9_CHICK	Q9w6u9 gallus gall
10	354	15.5	881	2 Q57519_XENLA	Q57519 xenopus lae
11	333	14.5	268	2 Q8TD78_HUMAN	Q8td78 homo sapien
12	332	14.5	288	2 Q6P36_HUMAN	Q9p36 homo sapien
13	332	14.5	349	2 Q9UHQ5_HUMAN	Q9uhj5 homo sapien
14	332	14.5	376	2 Q96P35_HUMAN	Q96p35 homo sapien
15	332	14.5	622	1 PRLR_HUMAN	P16471 homo sapien
16	332	14.5	622	1 Q5RAW0_PONPY	Q5raw0 pongo pygma
17	327.5	14.3	1010	2 Q7TQ89_RAT	Q7tcq9 rattus norv
18	323	14.1	857	2 Q5FC04_HUMAN	Q5fc04 homo sapien
19	323	14.1	918	1 IL6RB_HUMAN	P40189 homo sapien
20	317.5	13.9	917	1 IL6RB_MOUSE	Q00560 mus musculus
21	317.5	13.9	917	1 Q6PD15_MOUSE	Q6pd19 mus musculus
22	317	13.8	622	2 Q9N0J7_CALJA	Q9n0j7 callithrix
23	316	13.8	830	1 PRLR_COLLI	Q90374 columba liv
24	315	13.8	622	2 Q865V4_CEBAP	Q865v4 cebus apell
25	314.5	13.7	918	1 IL6RB_RAT	P40190 rattus norv
26	313	13.7	310	2 Q58DZ7_RAT	Q58dz7 rattus norv
27	313	13.7	610	1 PRLR_RAT	P05710 rattus norv
28	309.5	13.5	292	2 Q8C7G1_MOUSE	Q8c7g1 mus musculus
29	309.5	13.5	581	1 PRLR_SHEEP	Q46561 ovis aries
30	309.5	13.5	608	1 PRLR_MOUSE	Q08501 mus musculus
31	309.5	13.5	608	2 Q99JZ1_MOUSE	Q99jz1 mus musculus

32	308	13.4	460	2 Q7T220_CHICK	Q7t220 gallus gall
33	308	13.4	625	1 PRLR_PIG	Q6jta8 sus scrofa
34	308	13.4	831	1 PRLR_CHICK	Q04594 gallus gall
35	308	13.4	831	2 Q6QDA0_CHICK	Q6qda0 gallus gall
36	307	13.4	831	1 PRLR_MELGA	Q91094 meleagris g
37	306.5	13.4	581	1 PRLR_BOVIN	Q28172 bos taurus
38	304	13.3	581	1 PRLR_CEREL	Q28235 cervus elap
39	300.5	13.1	616	1 PRLR_RABIT	P14787 oryctolagus
40	294	12.8	611	2 Q9PTH9_XENLA	Q9pth9 xenopus lae
41	292.5	12.8	611	2 Q9IBF6_XENLA	Q9ibf6 xenopus lae
42	292.5	12.8	611	2 Q9PTI0_XENLA	Q9pti0 xenopus lae
43	291.5	12.7	604	2 Q6UAP8_TETNG	Q6uap8 tetraodon n
44	291	12.7	357	2 Q4SQD8_TETNG	Q4sqd8 tetraodon n
45	291	12.7	870	2 Q6UAN0_TETNG	Q6uan0 tetraodon n

ALIGNMENTS

RESULT 1
CRLF1_HUMAN STANDARD; PRT; 422 AA.
AC Q75462; Q9UHQ5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)
DE (CLF-1) (CYTOR5).
GN Name=CRLF1; Synonyms=ZCYTOR5; ORFNames=UNQ288/PRO327;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1] NUCLEOTIDE SEQUENCE, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND INDUCTION.
RC TISSUE=Fetal lung;
RX MEDLINE=98349389; PubMed=9686600;
RA Elson G.C.A., Graber P., Losberger C., Herren S., Gretener D.,
RA Menoud L.C., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.-F.;
RT "Cytokine-like factor-1, a novel soluble protein, shares homology with
members of the cytokine type I receptor family.";
J. Immunol. 161:1371-1379(1998).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
hematopoietic cytokine receptor domains.";
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Lok S., Presnell S.R., Jernberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA MEDLINE=28887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
[5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

CC RX TISSUE=Lymph;
CC RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
CC RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
CC RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
CC RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
CC RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
CC RA Villalon D.K., Muzny N.J., Sodergren E.J., Lu X., Gibbs R.A.,
CC RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
CC RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
CC RA Alakesh R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
CC RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
CC RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
CC RT "Generation and initial analysis of more than 15,000 full-length human
CC RL and mouse cDNA sequences.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC RN [6]
CC RP PROTEIN SEQUENCE OF 38-52.
CC RX PubMed=15340161; DOI=10.1110/ps.04682504;
CC RA Zhang Z., Hensel W.J.;
CC RT "Signal peptide prediction based on analysis of experimentally
CC RL verified cleavage sites.";
CC RL Protein Sci. 13:2819-2824(2004).
CC RN [7]
CC RP INTERACTIONS WITH CLC AND CNTFR.
CC RX MEDLINE=20423191; PubMed=10966616; DOI=10.1038/78765;
CC RA Elson G.C.A., Lelievre E., Guillet C., Chevalier S., Plun-Favreau H.,
CC RA Froger J., Suard I., de Coligny A.B., Delneste Y., Bonnefoy J.Y.,
CC RA Gauchat J.-F., Gascan H.;
CC RT "CLF associates with CLC to form a functional heteromeric ligand for
CC RT the CNTF receptor complex.";
CC RL Nat. Neurosci. 3:867-872(2000).
CC RN [8]
CC RP VARIANTS CISS HIS-81 AND ARG-374.
CC RX MEDLINE=22428294; PubMed=12509788;
CC RA Knappskog P.M., Majewski J., Livneh A., Nilsen P.T.E., Bringasli J.S.,
CC RA Ott J., Boman H.;
CC RT "Cold-induced sweating syndrome is caused by mutations in the CRLF1
CC RT gene.";
CC RL Am. J. Hum. Genet. 72:375-383(2003).
CC CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory
CC CC role in the immune system and during fetal development. May be
CC CC involved in nervous system development.
CC CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a
CC CC heteromeric complex with cardiotrophin-like cytokine (CLC); the
CC CC CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor
CC CC receptor (CNTFR).
CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- TISSUE SPECIFICITY: Highest levels of expression observed in
CC CC spleen, thymus, lymph node, appendix, bone marrow, stomach,
CC CC placenta, heart, thyroid and ovary. Strongly expressed also in
CC CC fetal lung.
CC CC -!- INDUCTION: Up-regulated in fibroblast primary cell cultures under
CC CC stimulation by IFN-gamma, TNF-alpha and IL-6.
CC CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC CC folding and thereby efficient intracellular transport and cell-
CC CC surface receptor binding.
CC CC -!- DISEASE: Defects in CRLF1 are the cause of cold-induced sweating
CC CC syndrome (CISS) [MIM:274301]. CISS is an autosomal recessive
CC CC disorder characterized by profuse sweating induced by cool
CC CC surroundings (temperatures of 7 to 18 degrees Celsius). Additional
CC CC abnormalities include a high-arched palate, nasal voice, depressed
CC CC nasal bridge, inability to fully extend the elbows and
CC CC kyphoscoliosis.
CC CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
CC CC subfamily.
CC CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.

CC CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC CC domain.
CC CC -----
CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use as long as its content is in no way modified and this statement is not
CC CC removed.
CC CC -----
CC DR EMBL; AF059293; AAC28335.1; -; mRNA.
CC DR EMBL; AF073515; AAD39681.1; -; mRNA.
CC DR EMBL; AF178684; AAD54385.1; -; mRNA.
CC DR EMBL; AY358291; AAO88658.1; -; mRNA.
CC DR EMBL; BC044634; AAH44634.1; -; mRNA.
CC DR HSSP; P40223; 1CD9.
CC DR Ensemble; ENSG0000006016; Homo sapiens.
CC DR HGNC; HGNC:2364; CRLF1.
CC DR MIM; 604237; -.
CC DR MIM; 272430; -.
CC DR GO; GO:0005615; C:extracellular space; TAS.
CC DR GO; GO:0019955; F:cytokine binding; IPI.
CC DR GO; GO:0004872; P:receptor activity; TAS.
CC DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. .); TAS.
CC DR InterPro; IPR002996; Cytokn recept_B/G.
CC DR InterPro; IPR003961; FN_III.
CC DR InterPro; IPR007110; Ig-like.
CC DR Pfam; PF00041; fn3; 2.
CC DR PROSITE; PS50853; FN3; 2.
CC DR PROSITE; PS50835; IG LIKE; FALSE NEG.
CC KW Direct protein sequencing; Disease mutation; Glycoprotein;
CC KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal.
CC FT SIGNAL 1 37
CC FT CHAIN 38 422 Cytokine receptor-like factor 1.
CC FT DOMAIN 38 131 Ig-like C2-type.
CC FT DOMAIN 134 229 Fibronectin type-III 1.
CC FT DOMAIN 234 334 Fibronectin type-III 2.
CC FT MOTIF 327 331 WSXWS motif.
CC FT MOD_RES 219 219 Phosphoserine (By similarity).
CC FT CARBOHYD 92 92 N-linked (GlcNAc. .) (Potential).
CC FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).
CC FT CARBOHYD 140 140 N-linked (GlcNAc. .) (Potential).
CC FT CARBOHYD 168 168 N-linked (GlcNAc. .) (Potential).
CC FT CARBOHYD 292 292 N-linked (GlcNAc. .) (Potential).
CC FT CARBOHYD 382 382 N-linked (GlcNAc. .) (Potential).
CC FT DISULFID 143 153 By similarity.
CC FT DISULFID 184 195 By similarity.
CC FT VARIANT 81 81 R -> H (in CISS).
CC FT VARIANT 374 374 L -> R (in CISS).
CC FT CONFLICT 240 240 /FTID=VAR_017865.
CC FT CONFLICT 240 240 D -> E (in Ref. 3).
CC SQ SEQUENCE 422 AA; 46302 MW; AD9DFCB01B84228 CRC64;
CC
CC Query Match 99.5%; Score 2279.5; DB 1; Length 422;
CC Best Local Similarity 99.8%; Pred No. 2.4e-166;
CC Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
CC
CC 1 MPAGRRGPAQAQARRPPPLP-LLLLVLGAPRAGGAHTAVISPDPTLLIGSSLLATC 59
CC 1 MPAGRRGPAQAQARRPPPLP-LLLLVLGAPRAGGAHTAVISPDPTLLIGSSLLATC 60
CC
CC 60 SVHGPPPGATAGLWTLNGRLPELSRVLTALANLNGSRQSGDNLVCHARD 119
CC 61 SVHGPPPGATAGLWTLNGRLPELSRVLTALANLNGSRQSGDNLVCHARD 120
CC
CC 120 GSILAGSLCYVGLPPEKPNVISCWKNMKDLICRWTPGAHGETFLHTNYSKYKLRWYG 179
CC 121 GSILAGSLCYVGLPPEKPNVISCWKNMKDLICRWTPGAHGETFLHTNYSKYKLRWYG 180
CC
CC 180 DNTCEYHTVGPSPHCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDLVVTTDPDPPD 239
CC 181 DNTCEYHTVGPSPHCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDLVVTTDPDPPD 240
CC Db

QY 240 VHSVRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLRLAG 299
 Db 241 VHSVRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSCLRLAG 300
 QY 300 LKPGTVYFVQVRCNPGIYVSGKAGIWSWSHPTAASPRSRPGPGGACPRGGEPS 359
 Db 301 LKPGTVYFVQVRCNPGIYVSGKAGIWSWSHPTAASPRSRPGPGGACPRGGEPS 360
 QY 360 GPVRELKQFLGWLKKGHCYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGP 419
 Db 361 GPVRELKQFLGWLKKGHCYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTARGP 420
 QY 420 AR 421
 Db 421 AR 422

RESULT 2
 ID CRLF1_MOUSE STANDARD; PRT; 425 AA.
 AC Q9JW58;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Cytokine receptor-like factor 1 precursor (Cytokine-like factor 1)
 DE (CLF-1) (Cytokine receptor-like molecule 3) (CRLM-3) (NR6).
 GN Name=Crlf1; Synonyms=Crlm3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX PubMed=10359701; DOI=10.1016/S0960-9822(99)80266-8;
 RA Alexander W.S., Rakar S., Robb L., Farley A., Willson T.A.,
 RA Zhang J.-G., Hartley L., Kikuchi Y., Kojima T., Nomura H.,
 RA Hasegawa M., Maeda M., Fabril L., Jachno K., Nash A., Metcalf D.,
 RA Nicola N.A., Hilton D.J.;
 RT "Suckling defect in mice lacking the soluble haemopoietin receptor
 NR6.";
 RL Curr. Biol. 9:605-608(1999).
 RN [3]
 RP PHOSPHORYLATION SITE SER-222.
 RX PubMed=15378723; DOI=10.1002/rcm.1604;
 RA Jin W.-H., Dai J., Zhou H., Xia Q.-C., Zou H.-F., Zeng R.;
 RA "Phosphoproteome analysis of mouse liver using immobilized metal
 affinity purification and linear ion trap mass spectrometry";
 RL Rapid Commun. Mass Spectrom. 18:2169-2176(2004).
 CC -!- FUNCTION: Cytokine receptor subunit, possibly playing a regulatory
 CC role in the immune system and during fetal development. May be
 CC involved in nervous system development (By similarity). Plays an
 CC essential role in the initiation and/or maintenance of suckling in
 CC neonatal mice.
 CC -!- SUBUNIT: Forms covalently linked di- and tetramers. Forms a
 CC heteromeric complex with cardiotrophin-like cytokine (CLC); the
 CC CRLF1/CLC complex is a ligand for the ciliary neurotrophic factor
 CC receptor (CNTFR) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Widely expressed in the embryo. Not detected
 CC in the brain of adult mice.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
 CC subfamily.
 CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 CC domain.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AB040038; BAA92777.1; -; mRNA.
 DR HSSP; P40223; 1CD9.
 DR Ensembl; ENSMUSG00000007888; Mus musculus.
 DR MGI; MGI:1340030; Crlf1
 DR CO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR002996; Cytokn_recept_B/G.
 DR InterPro; IPR003961; FN.III.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
 KW Glycoprotein; Immunoglobulin domain; Phosphorylation; Receptor;
 KW Repeat; Signal.
 FT SIGNAL 1 33 Potential.
 FT CHAIN 34 425 Cytokine receptor-like factor 1.
 FT DOMAIN 35 134 Ig-like C2-type.
 FT DOMAIN 137 232 Fibronectin type-III 1.
 FT DOMAIN 237 337 Fibronectin type-III 2.
 FT MOTIF 330 334 WSXWS motif.
 FT MOD_RES 222 222 Phosphoserine.
 FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 107 107 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 295 295 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
 FT DISULFID 146 156 By similarity.
 FT DISULFID 187 198 By similarity.
 SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 95.1%; Score 2178; DB 1; Length 425;
 Best Local Similarity 94.8%; Pred. No. 1.5e-158;
 Matches 402; Conservative 5; Mismatches 13; Indels 4; Gaps 2;

QY 1 MPAGRRGPAQSAARRPP-PLPLP---LLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL 56
 Db 1 MPAGRRGPAQSAARRPPRLSLWSPLLLCVLGVRGGSGAHTAVISPODPTLLIGSSLLQ 60

QY 57 ATCSVHGDPGATAEGLYWTNGRLPPPELSRVINASTLALANLNGSRQSGDNLVCH 116
 Db 61 ATCSVHGDPGATAEGLYWTNGRLPPPELSRVINASTLALANLNGSRQSGDNLVCH 120

QY 117 ARDGSILAGSCLYVGLPPEKPNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 176
 Db 121 ARDGSILAGSCLYVGLPPEKPNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180

QY 177 YQDNTCEYHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDLVVTTDP 236
 Db 181 YQDNTCEYHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSDDLTLDLVVTTDP 240

QY 237 PPDVHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSR 296
 Db 241 PPDVHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVVDVSNQTSR 300

QY 297 LAGLKPVTYFVQVRCNPGIYVSGKAGIWSWSHPTAASPRSRPGPGGACPRGGE 356
 Db 301 LAGLKPVTYFVQVRCNPGIYVSGKAGIWSWSHPTAASPRSRPGPGGACPRGGE 360

QY 357 PSSGPRRELKQFLGWLKKGHCYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTA 416
 Db 361 PSSGPRRELKQFLGWLKKGHCYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRGTA 420

QY 417 RGPA 420
 Db 421 RGPA 424


```

DR EMBL; CAAE01006801; CAF89355.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 22607 MW; 71F8E0B9998309F CRC64;

Query Match
Best Local Similarity 20.4%; Score 466.5; DB 2; Length 207;
Matches 100; Conservative 6; Mismatches 28; Indels 73; Gaps 2;

QY 227 DILDVVTTDPDPVHSRVGGLEDQLSVRWSPAPPALKFLOAKYQIRYRVDSVDWK-- 284
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 ECLPPVTTDPGSGTVSRVGGLEDQLSVRWSPAPPALKFLOAKYQIRYRVDSVDWKKE 60

QY 285 -----VVDVNSQTS 295
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 KSAFQDERAWTEPLCILGLRLVLMNEKYSVEAGPLQMALRLLPVLMVMDVGNQTS 120

QY 296 RIAGLKPQTVY-----FVQVRCNPFYIGSKKAGIWSWSHPT 333
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 121 RIAGLRPGTVYSRWDPGPAPQGTGSGSTAVSLPQVRCNPFYIGSKKAGIWSWSHPT 180

QY 334 AASTPRSERPGGGGACPRGGEPSG 360
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 181 AASTPHSGEPPLPAGPGRSLGAPESG 207

RESULT 7
Q4RD1 TETNG PRELIMINARY; PRT; 151 AA.
AC Q4RD1
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15947, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00037335001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RP "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01015947; CAG13471.1; -; Genomic_DNA.
DR NON_TER 151
FT SEQUENCE 151 AA; 16177 MW; 14AD74333AC67F90 CRC64;

Query Match
Best Local Similarity 17.7%; Score 406; DB 2; Length 151;
Matches 78; Conservative 17; Mismatches 37; Indels 6; Gaps 2;

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QY 25 LCVLGAPRAGSGAHTAVISPODPTLLIGSSILLATCSVHGDPGATAEGLYWTNGRLPP 84
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 20 VCV-----CGHPDVAEVSPPQDPVLPIGSSLTATCTLSPF-LRLSSALYWTNGETLPS 73

QY 85 ELSRVLNASTLALANLANLNGSRQSRSDNLVCHARDGSLAGSLYVGLPPEKPVNISCWS 144
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 74 STYGRGLGPHHTLSVTLHNLNGSRQSQSDNLVCHSSDGHVLGAGLACLYVGMPEKPVNLTCS 133

QY 145 KMKDLTCRWTPPGANGET 162
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 134 RNTKDLSCRWPRPGIGET 151

RESULT 8
Q4RD09 TETNG PRELIMINARY; PRT; 199 AA.
AC Q4RD09
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15948, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00037750001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bionet C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RP "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01015948; CAG13473.1; -; Genomic_DNA.
DR NON_TER 1
FT SEQUENCE 199 AA; 21734 MW; 299786CDFB24BDEB CRC64;

Query Match
Best Local Similarity 16.6%; Score 380; DB 2; Length 199;
Matches 73; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

QY 232 VTTDDPPDVHVSRVGGLEDQLSVRWSPAPPALKFLOAKYQIRYRVDSVDWKVDDVSN 291
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 34 VTTDDPPDVHVSRVGGLEDQLSVRWSPAPPALKFLOAKYQIRYRVDSVDWKVDDVSN 87

QY 292 QTSCLAGLKPQTVYFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRS 340
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 88 -----SVLWTVHFVQVRCNPFYIGSKKAGIWSWSHPTAASTPRS 128

RESULT 9
Q9W6U9_CHICK

```


RN NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=99182102; PubMed=10084611; DOI=10.1210/jc.84.3.1153;
RA Hu Z.-Z., Zhuang L., Meng J., Leonidires M., Dufau M.L.;
RT "The human prolactin receptor gene structure and alternative promoter
RT utilization: the generic promoter hPIII and a novel human promoter
RT hp(N).";
RL J. Clin. Endocrinol. Metab. 84:1153-1156 (1999).
RN [3]
RN NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Mammary carcinoma;
RA Kline J.B., Clevenger C.V.;
RT "Characterization of a novel and functional human prolactin receptor
RT isoform (delta-S1 PRLr) containing only one extracellular fibronectin-
RT like domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RN PARTIAL NUCLEOTIDE SEQUENCE (ISOFORM 3).
RC TISSUE=Mammary carcinoma;
RX MEDLINE=95286597; PubMed=7768908; DOI=10.1074/jbc.270.22.13133;
RA Fuh G., Wells J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
RT cancer cell lines.";
RL J. Biol. Chem. 270:13133-13137 (1995).
RN [6]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
RX MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;
RA Somers W., Ullrich M., de Vos A.M., Kossiakoff A.A.;
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";
RL Nature 372:478-481 (1994).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.
CC -!- INTERACTION:
CC P51956:NEK3; NbExp=1; IntAct=EBI-476182, EBI-476041;
CC P52735:VAV2; NbExp=1; IntAct=EBI-476182, EBI-297549;
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P16471-1; Sequence=Displayed;
CC Name=2; Synonyms=Delta-S1;
CC IsoId=P16471-2; Sequence=VSP_001720;
CC Name=3;
CC IsoId=P16471-3; Sequence=VSP_012620, VSP_012621;
CC Note=Soluble isoform that appears specific for the BT-474 breast
CC cancer cell line;
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.

CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation.
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 1
CC subfamily.
CC -!- SIMILARITY: Contains 2 fibronectin type-III domains.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M31661; AAA60174.1; -; mRNA.
DR EMBL; AF091870; AAD32032.1; -; Genomic_DNA.
DR EMBL; AF091863; AAD32032.1; JOINED; Genomic_DNA.
DR EMBL; AF091864; AAD32032.1; JOINED; Genomic_DNA.
DR EMBL; AF091865; AAD32032.1; JOINED; Genomic_DNA.
DR EMBL; AF091866; AAD32032.1; JOINED; Genomic_DNA.
DR EMBL; AF091867; AAD32032.1; JOINED; Genomic_DNA.
DR EMBL; AF091868; AAD32032.1; JOINED; Genomic_DNA.
DR EMBL; AF091869; AAD32032.1; JOINED; Genomic_DNA.
DR EMBL; AF349933; AAK32703.1; -; mRNA.
DR EMBL; BC059392; AAH59392.1; -; mRNA.
DR EMBL; S78505; AAB34470.1; -; mRNA.
DR PIR; A40144; A40144.
DR PDB; 1BP3; X-ray; B-25-235.
DR IntAct; P16471; -;
DR Ensembl; ENSG00000113494; Homo sapiens.
DR HGNC; HGNC:9446; PRLR.
DR MIM; 176761; -;
DR GO; GO:0005986; C:cell surface; IDA.
DR GO; GO:0042978; F:ornithine decarboxylase activator activity; ISS.
DR GO; GO:0004929; F:prolactin receptor activity; NAS.
DR GO; GO:0042803; F:protein homodimerization activity; NAS.
DR GO; GO:0005916; P:anti-apoptosis; NAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; NAS.
DR GO; GO:0007566; P:embryo implantation; TAS.
DR GO; GO:0007595; P:lactation; NAS.
DR GO; GO:0006694; P:steroid biosynthesis; NAS.
DR GO; GO:0042110; P:T cell activation; NAS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; IDA.
DR GO; GO:0042977; P:tyrosine phosphorylation of JAK2 protein; NAS.
DR InterPro; IPR002996; Cytokn_recept_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; HemtreceptL_F1.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR 3D-structure; Alternative splicing; Glycoprotein; Receptor; Repeat;
KW Signal; Transmembrane.
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FT CHAIN 25 622
FT TOPO_DOM 25 234
FT TRANSMEM 235 258
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FT DOMAIN 127 227
FT MOTIF 215 219
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FT CARBOHYD 104 104
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FT STRAND 224 225
SQ SEQUENCE 622 AA; 69506 MW; DB7FD0328608C787 CRC64;

Query Match 14.5%; Score 332; DB 1; Length 622;
Best Local Similarity 37.1%; Pred. NO. 9e-17;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

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Db 15 LFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWREGTDGG--LPTNYSLSYHREGETLM 72

QY 181 NTCEEYHTVGRSCHIPKD-LALFTPEYIWEATNRLGSARSDVLTLDILDVVTTDPPD 239
Db 73 HECPDYITGGPNSCHFGKQYTSWRTYIMVVRATNMGSSFSDELYVDVTYIVQDPPLE 132

QY 240 VHVSRVGGLEDQLSVRWV--SPPALKDF---LPQAKYQIRYVEDSDVKVVDVDSNQT 294
Db 133 LAV-EVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPKEAAWE-IHFAGQOTE 190

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Db 191 FKILSLHPGQKYLQVRCCKP-----DHGYNSANSPATFIQTP 227
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Search completed: April 11, 2006, 02:16:17
Job time : 125.397 secs

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OM protein - protein search, using sw model

Run on: April 11, 2006, 02:16:39 ; Search time 29.0921 Seconds
(without alignments)
1196.422 Million cell updates/sec

Title: US-09-037-657-44
Perfect score: 2290
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2279.5	99.5	422	2	US-09-944-457-32
3	2279.5	99.5	422	2	US-09-945-584-32
4	2279.5	99.5	422	2	US-09-944-944-32
5	2279.5	99.5	422	2	US-09-945-587-32
6	2275.5	99.4	422	2	US-09-071-224-2
7	2196	95.9	425	2	US-09-071-224-4
8	2188	95.5	410	2	US-09-521-335-12
9	2165	94.5	425	2	US-09-071-224-6
10	2164.5	94.5	448	2	US-09-120-601-6
11	2109	92.1	405	2	US-09-012-072-2
12	2109	92.1	405	2	US-09-120-601-2
13	2108	92.1	388	2	US-09-071-224-17
14	2095	91.5	407	2	US-09-521-335-13
15	2093.5	91.4	434	2	US-09-012-072-4
16	2093.5	91.4	434	2	US-09-120-601-4
17	2092	91.4	385	2	US-09-071-224-20
18	2045	89.3	385	2	US-09-071-224-19
19	2025	88.4	392	2	US-09-071-224-18
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21	2008	87.7	389	2	US-09-071-224-28
22	2008	87.7	389	2	US-09-071-224-29
23	2007	87.6	389	2	US-09-071-224-30
24	2006	87.6	389	2	US-09-071-224-24
25	2006	87.6	389	2	US-09-071-224-25
26	2006	87.6	389	2	US-09-071-224-27
27	2005	87.6	389	2	US-09-071-224-26

28	2004	87.5	389	2	US-09-071-224-31	Sequence 31, Appl
29	1645	71.8	303	2	US-09-071-224-23	Sequence 23, Appl
30	1641	71.7	303	2	US-09-071-224-21	Sequence 21, Appl
31	332	14.5	349	2	US-08-806-597A-14	Sequence 14, Appl
32	332	14.5	349	2	US-08-970-428A-14	Sequence 14, Appl
33	332	14.5	637	2	US-09-949-016-10128	Sequence 10128, A
34	329.5	14.4	1168	2	US-09-313-942-24	Sequence 24, Appl
35	329.5	14.4	1168	2	US-10-282-162-24	Sequence 24, Appl
36	325.5	14.2	599	2	US-09-000-145-2	Sequence 2, Appl
37	325	14.2	332	2	US-09-313-942-10	Sequence 10, Appl
38	325	14.2	332	2	US-10-282-162-10	Sequence 10, Appl
39	324.5	14.2	1158	2	US-09-313-942-26	Sequence 26, Appl
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44	323	14.1	488	2	US-08-864-564A-5	Sequence 5, Appl
45	323	14.1	488	2	US-09-094-410-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-866-028-32
; Sequence 32, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-32

Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 1.2e-210;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 420 AR 421
Db 421 AR 422

RESULT 2

US-09-944-457-32
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; Patent No. 6734288
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/944,457
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
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; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
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; PRIOR FILING DATE: December 12, 1997
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; PRIOR APPLICATION NUMBER: 60/069,702
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; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6734288ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-457-32
Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 1.2e-210;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVTSPQDPTLLIGSSLLATC 59
Db 1 MPAGRRGPAQAQARRPPPLP-LLLLCVLGAPRAGSGAHTAVTSPQDPTLLIGSSLLATC 60
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Db 421 AR 422

RESULT 3

US-09-945-584-32
; Sequence 32, Application US/09945584
; Patent No. 6908993
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Batstein, David
; APPLICANT: Batson, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Eileen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,584
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
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; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
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; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086
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; PRIOR APPLICATION NUMBER: 60/074,092
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; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
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; PRIOR FILING DATE: December 16, 1998
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; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
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; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-584-32

Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 1.2e-210;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MPAGRRGPAAGSARRPPPLP-LIALLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59
Db 1 MPAGRRGPAAGSARRPPPLP-LIALLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
QY 60 SVHGDPPGATAGLYWTLNGRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
Db 61 SVHGDPPGATAGLYWTLNGRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHGTFLHTNYSLKYKLRWYQ 179
Db 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAGHGTFLHTNYSLKYKLRWYQ 180

QY 180 DNTCEYHTVGHPSCHIPKDLALFTPEYEWVEATNRLGARSVDLTLDILDVVTTDDPPD 239
Db 181 DNTCEYHTVGHPSCHIPKDLALFTPEYEWVEATNRLGARSVDLTLDILDVVTTDDPPD 240
QY 240 VHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 299
Db 241 VHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVSNQTSCLAG 300
QY 300 LKPGTVYFVQVRCNPPGFIYGSKKAGIWSHSHPTAASTPRSERPGGGACBPRGGEPS 359
Db 301 LKPGTVYFVQVRCNPPGFIYGSKKAGIWSHSHPTAASTPRSERPGGGACBPRGGEPS 360
QY 360 GPVRELKQFLGWLKHCAYCSNLSFRLYDQWRAWMQSKHTRNQDREGILPDSGRGTARGP 419
Db 361 GPVRELKQFLGWLKHCAYCSNLSFRLYDQWRAWMQSKHTRNQDREGILPDSGRGTARGP 420
QY 420 AR 421
Db 421 AR 422
RESULT 5
US-09-945-587-32
; Sequence 32, Application US/09945587
; Patent No. 6936254
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/1146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6936254ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-945-587-32

Query Match 99.5%; Score 2279.5; DB 2; Length 422;
Best Local Similarity 99.8%; Pred. No. 1.2e-210;
Matches 421; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRRGPAQSAARRPPPLLP-LLLLCVLGAPRAGSGAHTAVTSPDPTLLIGSSLLATC 59
Db 1 MPAGRRGPAQSAARRPPPLLP-LLLLCVLGAPRAGSGAHTAVTSPDPTLLIGSSLLATC 60
QY 60 SVHGDPGPGATAGLYWTLNGRELPPPELSRVLTASTLALANLNGSRQSGDNLVCHARD 119
Db 61 SVHGDPGPGATAGLYWTLNGRELPPPELSRVLTASTLALANLNGSRQSGDNLVCHARD 120
QY 120 GSIILAGSCLYVCLPPEKPVNISCWNKMDLTCRWTPGAHGETFLHTNYSLKVKLRWYQG 179
Db 121 GSIILAGSCLYVCLPPEKPVNISCWNKMDLTCRWTPGAHGETFLHTNYSLKVKLRWYQG 180

QY 180 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLDDVTTDPPD 239
DB 181 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLDDVTTDPPD 240
QY 240 VHSVGVGLEDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 299
DB 241 VHSVGVGLEDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 300
QY 300 LKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGACPRGGEPS 359
DB 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGACPRGGEPS 360
QY 360 GVPVRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 419
DB 361 GVPVRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 6

US-09-071-224-2
; Sequence 2, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal

US-09-071-224-2

Query Match 99.4%; Score 2275.5; DB 2; Length 422;

Best Local Similarity 99.5%; Pred. No. 2.9e-210;
Matches 420; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MPAGRGPAQASARRPPPLP-LLLL CVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 59
DB 1 MPAGRGPAQASARRPPPLP-LLLL CVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
QY 60 SVHGDPPGATAGLYWTNLNGRRLPELSRVLNASTLALANLNGSRORSNDLVCHARD 119
DB 61 SVHGDPPGATAGLYWTNLNGRRLPELSRVLNASTLALANLNGSRORSNDLVCHARD 120
QY 120 GSILAGSCLYVGLPEKPNISCSKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQG 179
DB 121 GSILAGSCLYVGLPEKPNISCSKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQG 180
QY 180 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLDDVTTDPPD 239
DB 181 DNTCEYHTVGPSSCHIPKDLALFTPEYIWEATNRLGARSVDLTDLDDVTTDPPD 240
QY 240 VHSVGVGLEDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 299
DB 241 VHSVGVGLEDQLSVRWVSPALDKDFLFOAKYQIRYRVEDSVWKVDDVSNQTSCLAG 300
QY 300 LKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGACPRGGEPS 359
DB 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSRPFGGACPRGGEPS 360
QY 360 GVPVRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 419
DB 361 GVPVRELKQFLGWLKHHAYCSNLSFRLYDQWRANWQKSHKTRNDEGILPSGRRGTARGP 420
QY 420 AR 421
DB 421 AR 422

RESULT 7

US-09-071-224-4
; Sequence 4, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 425 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-071-224-4

Query Match 95.9%; Score 2196; DB 2; Length 425;

Best Local Similarity 100.0%; Pred. No. 1.3e-202;

Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRGPAQAARRPPPLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCS 60

DB 1 MPAGRGPAQAARRPPPLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCS 60

QY 61 VHGDPGATAGLYWTNGRLPPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120

DB 61 VHGDPGATAGLYWTNGRLPPPELSRVLNASTLALANLNGSRQSGDNLVCHARDG 120

QY 121 SILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQD 180

DB 121 SILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQD 180

QY 181 NTCEEYHTVGPCHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVVTTDPPPDV 240

DB 181 NTCEEYHTVGPCHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVVTTDPPPDV 240

QY 241 HVSVRGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAGL 300

DB 241 HVSVRGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAGL 300

QY 301 KPGTVYFVQVRCNPFYIGSKKAGIWESEHPTAASTPRSERPGGGGACPRGGPSSG 360

DB 301 KPGTVYFVQVRCNPFYIGSKKAGIWESEHPTAASTPRSERPGGGGACPRGGPSSG 360

QY 361 PVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ 403

DB 361 PVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ 403

RESULT 8

US-09-521-335-12

Sequence 12, Application US/09521335

Patent No. 6800460

GENERAL INFORMATION:

APPLICANT: Oppmann, Birgit

APPLICANT: Timans, Jacqueline C.

APPLICANT: Kastelein, Robert A.

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods

FILE REFERENCE: DX0935K

CURRENT APPLICATION NUMBER: US/09/521,335

CURRENT FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 410

TYPE: PRT

ORGANISM: primate

US-09-521-335-12

Query Match

Best Local Similarity 95.5%; Score 2188; DB 2; Length 410;

Matches 405; Conservative 1; Mismatches 0; Indels 4; Gaps 2;

QY 1 MPAGRGPAQAARRPPPLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 59

DB 1 MPAGRGPAQAARRPPPLPLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

QY 60 SVHGDPGATAGLYWTNGRLPPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119

DB 61 SVHGDPGATAGLYWTNGRLPPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120

QY 120 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQ 179

DB 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQ 180

QY 180 DNTCEEYHTVGPCHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVVTTDPPPD 239

DB 181 DNTCEEYHTVGPCHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVVTTDPPPD 240

QY 240 HVSVRGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAG 299

DB 241 HVSVRGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVDMKVVDVSNQTSCLAG 300

QY 300 LKPGTVYFVQVRCNPFYIGSKKAGIWESEHPTAASTPRSERPGGGGACPRGGPSS 359

DB 301 LKPGTVYFVQVRCNPFYIGSKKAGIWESEHPTAASTPRSERPGGGGACPRGGPSS 360

QY 360 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILP 409

DB 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAWMQSHKTRNQ---VLP 407

RESULT 9

US-09-071-224-6

Sequence 6, Application US/09071224

Patent No. 6271343

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Presnell, Scott R.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Gilbert, Teresa

APPLICANT: Foster, Donald C.

APPLICANT: Adams, Robyn L.

APPLICANT: Lehner, Joyce M.

TITLE OF INVENTION: MAMMALIAN ZCYTORS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics

STREET: 1201 Eastlake Ave East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,224

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 425 amino acids

TYPE: amino acid

QY 383 SFRLYDQWRAMQKSHKTRNQDEGILPSGRRGTARGPA 420
Db 367 SFRLYDQWRAMQKSHKTRNQDEGILPSGRRGTARGPA 404

RESULT 12

US-09-120-601-2
; Sequence 2, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-120-601-2

Query Match 92.1%; Score 2109; DB 2; Length 405;
Best Local Similarity 96.5%; Pred. No. 2.9e-194;
Matches 384; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 23 LLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRL 82
Db 7 LLLCVLGVPRGSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRL 66
QY 83 PPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPNVISC 142
Db 67 PSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPNVISC 126
QY 143 WSKNNKDLTCTWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLAL 202
Db 127 WSRNKKDLTCTWTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLAL 186
QY 203 PTPHEIWEATNRLGASRDLVTLDLVVTDDPPDVHVSVRVGLGDLQSVRWVSPPAL 262
Db 187 PTPHEIWEATNRLGASRDLVTLDLVVTDDPPDVHVSVRVGLGDLQSVRWVSPPAL 246
QY 263 KDFLFOAKYQIRYVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFYIGSKK 322
Db 247 KDFLFOAKYQIRYVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFYIGSKK 306
QY 323 AGIWESEWSHPTAASPRSERPGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNL 382
Db 307 AGIWESEWSHPTAASPRSERPGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNL 366
QY 383 SFRLYDQWRAMQKSHKTRNQDEGILPSGRRGTARGPA 420
Db 367 SFRLYDQWRAMQKSHKTRNQDEGILPSGRRGTARGPA 404

RESULT 13

US-09-071-224-17
; Sequence 17, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jeilberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-224-17

Query Match 92.1%; Score 2108; DB 2; Length 388;
Best Local Similarity 99.5%; Pred. No. 3.4e-194;
Matches 386; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 34 GSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRLPPELSRVLNAS 93
Db 1 GSGAHTAVISQDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRLPPELSRVLNAS 60
QY 94 TLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPNVISCWKNMKDLTCL 153
Db 61 TLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPNVISCWKNMKDLTCL 120
QY 154 WTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLALFTPYEIVWEAT 213
Db 121 WTPGAHGETFLHTNYSKYKLRWYQDNTCEYHTVGPCHIPKDLALFTPYEIVWEAT 180
QY 214 NRLGASRDLVTLDLVVTDDPPDVHVSVRVGLGDLQSVRWVSPPALKDFLFOAKYQI 273
Db 181 NRLGASRDLVTLDLVVTDDPPDVHVSVRVGLGDLQSVRWVSPPALKDFLFOAKYQI 240
QY 274 RYRVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFYIGSKKAGIWESEWSHPT 333
Db 241 RYRVEDSVDMKVDDVSNQTSCLAGLKPVTYFVQVRCNPFYIGSKKAGIWESEWSHPT 300
QY 334 AASTPRSERPGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNLSFRLYDQWRAM 393
Db 301 AASTPRSERPGGGACPRGGEPSGVPVRELKQFLGWLKCHAYCSNLSFRLYDQWRAM 360
QY 394 MOKSHKTRNQDEGILPSGRRGTARGPA 421
Db 361 MOKSHKTRNQDEGILPSGRRGTARGPA 388

RESULT 14

US-09-521-335-13
; Sequence 13, Application US/09521335
; Patent No. 6800460
; GENERAL INFORMATION:

```
; APPLICANT: Oppmann, Birgit
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/09/521,335
; CURRENT FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-09-521-335-13

Query Match          91.5%; Score 2095; DB 2; Length 407;
Best Local Similarity 95.1%; Pred. No. 6.4e-193;
Matches 386; Conservative 5; Mismatches 11; Indels 4; Gaps 2;

QY 18 PLLPL---LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSVHGDPFGATAEGLY 74
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Db 2 PLSSLSPLLLCVLGVPRGSGAHTAVISPDPTLLIGSSLLQATCSIHGDTFGATAEGLY 61
   |||||

QY 75 WTLNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPP 134
   |||||
Db 62 WTLNGRRL--PSLSRLANTSTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPP 120
   |||||

QY 135 EKPVNISCSWKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP HSC 194
   |||||
Db 121 EKPVNISCSWKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP HSC 180
   |||||

QY 195 HIPKDLALFTPEYIWEATNRLGARSVDLTLDVVTDDPPDVHVSRVGGLDQLSV 254
   |||||
Db 181 HIPKDLALFTPEYIWEATNRLGARSVDLTLDVVTDDPPDVHVSRVGGLDQLSV 240
   |||||

QY 255 RVVSPALKDFLEQAKYQIRYRVEDSDVKVDDVSNQTSCLAGLKPGTVYFVQVRCNP 314
   |||||
Db 241 RVVSPALKDFLEQAKYQIRYRVEDSDVKVDDVSNQTSCLAGLKPGTVYFVQVRCNP 300
   |||||

QY 315 FGIGSKKAGIWESEHPTAASPTSRERPGGGACEPRGSGPSPVRRRLKQFLGWLK 374
   |||||
Db 301 FGIGSKKAGIWESEHPTAASPTSRERPGGGACEPRGSGPSPVRRRLKQFLGWLK 360
   |||||

QY 375 KHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPSGRGTARGPA 420
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Db 361 KHAYCSNLSFRLYDQWRAMWQKSHKTRNQDEGILPSGRGTARGPA 406
   |||||

RESULT 15
US-09-012-072-4
; Sequence 4, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-012-072-4

Query Match          91.4%; Score 2093.5; DB 2; Length 434;
Best Local Similarity 94.4%; Pred. No. 9.9e-193;
Matches 389; Conservative 0; Mismatches 0; Indels 23; Gaps 2;

QY 15 RPPPLLP-LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSVHGDPFGATAEGL 73
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Db 1 RPPPLLP-LLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSVHGDPFGATAEGL 60
QY 74 WTLNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLP 133
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Db 61 WTLNGRRLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLP 120
   |||||
QY 134 EKPVNISCSWKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP HSC 193
   |||||
Db 121 EKPVNISCSWKMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEEYHTVGP HSC 180
   |||||
QY 194 CHIPKDLALFTPEYIWEATNRLGARSVDLTLDVVTDDPPDVHVSRVGGLDQLSV 231
   |||||
Db 181 CHIPKDLALFTPEYIWEATNRLGARSVDLTLDVVTDDPPDVHVSRVGGLDQLSV 240
   |||||
QY 232 VTTDPPDVHVSRVGGLDQLSVRVVSPALKDFLEQAKYQIRYRVEDSDVKVDDVSN 291
   |||||
Db 241 VTTDPPDVHVSRVGGLDQLSVRVVSPALKDFLEQAKYQIRYRVEDSDVKVDDVSN 300
   |||||
QY 292 QTSCLAGLKPGTVYFVQVRCNPPFGIYGSKKAGIWESEHPTAASPTSRERPGGGACE 351
   |||||
Db 301 QTSCLAGLKPGTVYFVQVRCNPPFGIYGSKKAGIWESEHPTAASPTSRERPGGGACE 360
   |||||
QY 352 PRGGEPSGPPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQ 403
   |||||
Db 361 PRGGEPSGPPVRRRLKQFLGWLKKHAYCSNLSFRLYDQWRAMWQKSHKTRNQ 412
   |||||

Search completed: April 11, 2006, 02:19:00
Job time : 30.0921 secs
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76560
STIC-Biotech/ChemLib

184613

11/9

From: Woodward, Michael
Sent: Friday, April 07, 2006 1:46 PM
To: STIC-Biotech/ChemLib
Cc: Hamud, Fozia
Subject: FW: rush search 09/037, 657

Please put in ~~rush~~ queue.

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-----Original Message-----

From: Hamud, Fozia
Sent: Friday, April 07, 2006 1:38 PM
To: Woodward, Michael
Cc: Chan, Christina
Subject: rush search 09/037, 657

Hi Mr. Woodward,
Would you kindly approve this rush search? It is a very old case in my docket. The claims are allowable. However, Applicant is running out of time by Thursday the 13th of April. An interference search must be done before then. thanks.

Stic:
Kindly search SEQ ID NOs: 13, 15 and 44 of 09/037,657 against commercial and interference data bases. Thank you very much.

FOZIA HAMUD
PATENT EXAMINER
ART UNIT 1647
ROOM:REM 4D64
MAIL BOX: REM 4C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
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Type of Search
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S/L: _____ Oligomer: _____
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Inventor: _____ Litigation: _____

Vendors and cost where applicable
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Other (Specify): _____

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